

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 21, 2006, 13:11:04 ; Search time 26 Seconds

(without alignments)
529.727 Million cell updates/sec

Title: US-10-664-421-1

Perfect score: 1670

Sequence: 1 MLLSKINSLAHLRAAPCNLDL.....LLPQETAETHLSLSPGPK 313

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New.*
1: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB_PEP.*
2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB_PEP.*
5: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
6: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB_PEP.*
7: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB_PEP.*
8: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	869.5	52.1	311	US-11-103-065-2	Sequence 2, Appli
2	384.5	23.0	256	US-10-877-346-74	Sequence 74, Appl
3	376	22.5	950	US-10-501-035-357	Sequence 357, App
4	368.5	22.1	631	US-11-241-056-11	Sequence 11, Appl
5	366	21.9	504	US-11-087-099-9816	Sequence 9816, Ap
6	364.5	21.8	256	US-10-877-346-72	Sequence 72, Appl
7	364.5	21.8	256	US-11-113-424-183	Sequence 183, Appl
8	356	21.3	514	US-11-087-099-11500	Sequence 11500, A
9	352	21.1	512	US-11-087-099-3997	Sequence 3997, Ap
10	352	21.1	514	US-11-087-099-3612	Sequence 3612, Ap
11	348.5	20.9	619	US-11-087-099-12402	Sequence 12402, A
12	348	20.8	472	US-11-087-099-11838	Sequence 11838, A
13	342.5	20.5	651	US-10-770-726-67	Sequence 67, Appl
14	342.5	20.5	651	US-11-177-138-10	Sequence 10, Appl
15	342	20.5	464	US-11-096-568A-22124	Sequence 22124, A
16	341	20.4	513	US-11-087-099-11726	Sequence 11726, A
17	340	20.4	620	US-11-087-099-3898	Sequence 3898, Ap
18	339.5	20.3	504	US-11-087-099-12331	Sequence 12331, A
19	339	20.3	713	US-10-995-561-881	Sequence 881, App
20	339	20.3	729	US-10-995-561-878	Sequence 878, App
21	339	20.3	737	US-10-995-561-880	Sequence 880, App
22	339	20.3	744	US-10-995-561-876	Sequence 876, App
23	339	20.3	753	US-10-995-561-877	Sequence 877, App
24	337.5	20.2	689	US-10-204-639-17	Sequence 17, Appl
25	336.5	20.1	445	US-11-096-568A-32575	Sequence 32575, A

26	336.5	20.1	448	7	US-11-096-568A-18364	Sequence 18364, A
27	333.5	20.0	1518	7	US-11-087-099-1886	Sequence 1886, Ap
28	332	19.9	439	7	US-11-096-568A-20431	Sequence 20431, A
29	332	19.9	443	7	US-11-096-568A-20430	Sequence 20430, A
30	328.5	19.7	715	6	US-10-204-639-65	Sequence 65, Appl
31	328	19.6	277	7	US-11-151-601-4	Sequence 4, Appl
32	327	19.6	358	6	US-10-979-095-6	Sequence 6, Appl
33	327	19.6	582	7	US-11-096-568A-32895	Sequence 32895, A
34	326.5	19.6	765	7	US-11-087-099-905	Sequence 905, App
35	325.5	19.5	278	6	US-10-055-877-149	Sequence 149, App
36	325.5	19.5	278	7	US-11-103-065-4	Sequence 4, Appl
37	325.5	19.5	278	7	US-11-151-601-10	Sequence 10, Appl
38	325.5	19.5	339	7	US-11-172-740-987	Sequence 987, App
39	324	19.4	401	7	US-11-087-099-6642	Sequence 6642, Ap
40	323	19.3	473	7	US-11-087-099-8865	Sequence 8865, Ap
41	323	19.3	513	7	US-11-087-099-7631	Sequence 7631, Ap
42	323	19.3	876	7	US-11-087-099-10193	Sequence 10193, A
43	322.5	19.3	611	7	US-11-087-099-8358	Sequence 8358, Ap
44	321.5	19.3	602	7	US-11-087-099-11542	Sequence 11542, A
45	319.5	19.1	432	7	US-11-096-568A-32576	Sequence 32576, A

ALIGNMENTS

RESULT 1

US-11-103-065-2
; Sequence 2, Application US/11103065
; Publication No. US20050282189A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel E., Jose M.
; TITLE OF INVENTION: 2150, Human Protein Kinase Family
; TITLE OF INVENTION: Member and Uses Therefor
; FILE REFERENCE: MPI2001-137PIENM
; CURRENT APPLICATION NUMBER: US/11/103,065
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: US/10/184,563
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,702
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-103-065-2

Query Match 52.1%; Score 869.5; DB 7; Length 311;
Best Local Similarity 58.4%; Pred. No. 6.9e-72;
Matches 167; Conservative 39; Mismatches 75; Indels 5; Gaps 2;
QY 28 GKEKEPLESQYQVGPLLGGFGSVYSGIRVSDNLPVAIKHVEKORISDWGELPNCGRVP 87
DB 22 GKDRFAEAYRLGLPLGKGGGTTFAGHLTDRLQVAIKVPRNVLGWSPLSDSVTCP 81
QY 88 MEVLLKKVSS--GFSGVIRLLDWFEPDSFVILIERPEPVDLFDFFITERGALQBELAR 145
DB 82 LEVALLKVGAGGHPGVIRLLDWFETQGFVLRPLPAQDLFDYITEKGPLGEGPSR 141
QY 146 SFFQVLEAVRHCHNGCVLHRDIKDENILIDLNRGELKLDIFGSGALLKDYVYTFDGTGR 205
DB 142 CFQGVAAIQCHSRGVVHRDIKDENILIDLRRGCAKLDIFGSGALLHDEPYTDFDGTGR 201
QY 206 VYSPPEWIRYHYHGRSAVWSLGIILYDMVCGDIPFEHDEETIRGQVFFRQVRSQCQH 265
DB 202 VYSPPEWIRYHYHALPATVNSLGIILYDMVCGDIPFERDQELLEAEHLFFPAHVSDDCA 261
QY 266 LIRWCLALRPSDRPTFEETIQNHPPWQDVLPLPOETAIHLHLSLSPG 311
DB 262 LIRRCCLAPKPSRPSLEILLDPWQ---TPAEDVLPNPSKGGPAP 304

RESULT 2
US-10-877-346-74
; Sequence 74, Application US/10877346
; Publication No. US20060014153A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shinketsu, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Protein kinase
; OTHER INFORMATION: domain Consensus Sequence
US-10-877-346-74
Query Match 23.0%; Score 384.5; DB 6; Length 256;
Best Local Similarity 37.0%; Pred. No. 1.3e-27;
Matches 98; Conservative 46; Mismatches 98; Indels 23; Gaps 9;
38 YQVGPLLGSGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVS 97
1 YELGKGLSGAGFKVYKGRKDKTGETVAIKILKGRSLSE-----KKGRFLREIQILRLIS 55
98 SGFSGVIRLLDWFERPDSFVILIRPEPVQDLFDFTITERG-ALOBELARSPFQVLEAVR 156
56 --HPNIVRLGLGVFEEDHHYLVWYNEG-GDLFDVLRNGLLSSEKAKKIALQILRGLE 112
157 HCHNCGLVRDVKDENILIDLNRGELKLDLFGSGALLKDTVY---TDFDGTFRVYSPPEVI 213
113 YLHRSRGIVRDLKPENILLDEN-GTVKIADFGLARKLESSSYEKLTTFTVGTPEYMAPEVL 171

214 RYRHYGRSAAVWSGLILLYDMVCGDIPF---EHDDEIIRGVQVFRQV-----SSEQC 264
172 EGRGYSSK-VDVWSLGVILYELLTGKLFPGIDPLEELFRIKERPRLLPLPPNCSEELK 230
265 HLIRWCLALRPSDRPTFEEIQNHWP 289
231 DLIKKLKNKPEKPTAKEILNHPW 255
RESULT 3
US-10-501-035-357
; Sequence 357, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 357
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-357
Query Match 22.5%; Score 376; DB 6; Length 950;
Best Local Similarity 32.4%; Pred. No. 4.3e-26;
Matches 89; Conservative 50; Mismatches 114; Indels 22; Gaps 7;
38 YQVGPLLGSGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVS 97
44 YDIEGTGKGNFVAVKLRHRTKTEVAIKIDKSQ-----DAVNLEKIRVQIMKMLD 99
98 SGFSGVIRLLDWFERPDSFVILIRPEPVQDLFDFTITERGALQEBELARSPFQVLEAVRH 157
100 --HPHIIKLYQVMTKSMYLVTYAKN-GBIFDYLANHGRLNSEARRKFWQILSAVDY 156
158 HCHNCGLVRDVKDENILIDLNRGELKLDLFGSGALLKDTVYDFTDGTFRVYSPPEVIRH 216
157 CHGRKIVHRDLKAENLLLD-NNMNIKIADFGFNGFRKSGELLATWCGSPPPYAAPVFEQG 215
217 RYHGRSAAVWSGLILLYDMVCGDIPFHD-----EETIRGVQVFRQVSSCOHLIRMC 270
216 QYEGPQLDINSGVYLVVLCALPFDGPTLPILRQVLEGRFRIPYFMSEDCHEHLIRRM 275
271 LALRPSDRPTFEEIQNHWP-----QDVLLPQE 298
276 LVLDPSKRLTTAQIKHKKWMLIEVPVQRPVLPQE 310
RESULT 4
US-11-241-056-11
; Sequence 11, Application US/11241056
; Publication No. US20060024807A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-US
; CURRENT APPLICATION NUMBER: US/11/241,056
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US/09/980,464
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 36

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-241-056-11

Query Match          22.1%; Score 368.5; DB 7; Length 631;
Best Local Similarity 33.4%; Pred. No. 1.2e-25;
Matches 99; Conservative 46; Mismatches 116; Indels 33; Gaps 9;

QY 22 ATKLPQKEKEP-----LESQVQVGLSGGFGSVSGIRVSDNLPV 64
Db 24 ARPLADGLKSPKPLMKKQAVKRRHHKHNLRHYEFLETGKTYGKVKA-RESSGLRV 82
QY 65 AIKHVKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWDPERPDSFVILIERPE 124
Db 83 AIKSIRKDKIKRQDL---LHIRREIEMS--SLNHPHIIAIEHVPENSKIVIVMEYAS 137
QY 125 PVQDLDFITERGALQOEELARSFFMQVLEAVRHCHNCGVLRDIDKDNILIDLNRGELKL 184
Db 138 R-GDLVDYISERPLSERDARHPFQIVSALHYCHQNGIVHRDLKLENILLDAN-GNIKI 195
QY 185 IDPG-SCALLKOTVYTFDQTRVYSPPEWIRYHGRSAAVMSLGLLYDMVCGDIPFE 243
Db 196 ADFGLSNLYHKGFELQTFGSPLYASPEIVNGKPYVGPVDSWSLGLVILYLVHGTMPD 255
QY 244 HDB-----EIRGQVFFRQRVSSECOHLRWCLALRPSDRPTFBIQHPWM 290
Db 256 QGDHKLTVQISNGAYREPPKPSDAC-GLIRLLWMVNPTRATLEDVASHWVV 307

RESULT 5
US-11-087-099-9816
; Sequence 9816, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9816
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Cucumis sativus
US-11-087-099-9816

Query Match          21.9%; Score 366; DB 7; Length 504;
Best Local Similarity 34.4%; Pred. No. 1.6e-25;
Matches 90; Conservative 51; Mismatches 105; Indels 16; Gaps 8;

QY 38 YQVGPLLGGGFGSVSGIRVSDNLPVAKHKVEKDRISDWGELPNCGRVPMVEVLLKKVS 97
Db 8 YKLGKTLGIGSGFGKVIKAEHALTGHKVAIKLNRRKIKN---LDMEKVRREIKILRLPM 64
QY 98 SGFGSVIRLLDWERPDSFVILIERPEPVQDLDFITERGALQOEELARSFFMQVLEAVRH 157
Db 65 --HPHILRYEVIETSDIYVMEYKS-GELEFDYIVEKGRQEDEARNFQOIISGVY 121
QY 158 CHNCGVLHRDIDKDNILIDLNRGELKLIDFGSGALLKOTVYTFD-GTRVYSPPEWIRYH 216
Db 122 CHRNMMVHRDLKPENLLD-SKCNVKIADFGLSNMRDGHFLKTSKCSPNYAAPEVISG 180
QY 217 RYHGRSAAVMSLGLLYDMVCGDIPFEHDEI-----IRGQVF-PRQRVSSECOHLIRW 269
Db 181 LVAGPEVDVMSCGVILYALCGTLPPD-DENIPNLFKIKGGIYTLPSHLSGARELIPS 239
QY 270 CLALRPSDRPTFBIQHPWMQ 291
Db 240 MLVVDPMKRIITPEIRQHWFQ 261

RESULT 6
US-10-877-346-72
; Sequence 72, Application US/10877346
; Publication No. US20060014153A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenna
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Rameesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shinkets, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Serine/Threonine protein kinase Consensus
; OTHER INFORMATION: Sequence
US-10-877-346-72

Query Match          21.8%; Score 364.5; DB 6; Length 256;
Best Local Similarity 33.3%; Pred. No. 8.9e-26;
Matches 89; Conservative 55; Mismatches 96; Indels 27; Gaps 8;

QY 38 YQVGPLLGGGFGSVSGIRVSDNLPVAKHKVEKDRISDWGELPNCGRVPMVEVLLKKVS 97
Db 1 YELLEVLGKAGKGYLARDKTKGLVAKVKKEL----KKKKERILRIKILKKLD 56
QY 98 SGFGSVIRLLDWERPDSFVILIERPEPVQDLDFITERGALQOEELARSFFMQVLEAVRH 157
Db 57 --HPNIVKLYDVFEDDDKLYLVMEYCEG-GDLFLLKKRGLSEDEARFYARQILSALEY 113
QY 158 CHNCGVLHRDIDKDNILIDLNRGELKLIDFGSGALLKD--TVYTFDGTFRVYSPPEWIRY 215
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Db 114 LHSQGIHRLDKPENILLD-SDGHVKLADFLGAKQLDSGTLTTTFVGTPEYMAPE-VLL 171
QY 216 HRYHGRSAAWSGLILYDMVCGDIPFEHDEEILIRQVFRQ-----RVSSSE 262
Db 172 KGKYGKAVDWSGLVILYELLTKGPPFGDDQLL---ALFKKIGKPPPPPPPEWKISPE 228
QY 263 COHLIRWCLALRPSDRPTFEEIQNHWP 289
Db 229 AKDLIKKLVKDPKRLTAEALEHPF 255

RESULT 7

US-11-113-424-183
; Sequence 183, Application US/11113424
; Publication No. US20050280713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; PRIOR FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 183
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-11-113-424-183

Query Match 21.8%; Score 364.5; DB 7; Length 256;
Best Local Similarity 33.3%; Pred. No. 8.9e-26;
Matches 89; Conservative 55; Mismatches 96; Indels 27; Gaps 8;

QY 38 YQVGPLLAGSGFGSVYSGIRVSDNLPVAIKHVKDKRISDWGELPNGTRVPMEVVLLKKVYS 97
Db 1 YELLEVGLGAGFKVYLARDKKTGKLVAKVKKKEKL-----KKKKRILREIKILKULD 56
QY 98 SGFSGVIRLLDMFERPDSFVLILRPEPVQDLDFDITERGALQOEELARSFFQVLEAVRH 157
Db 57 --HPNIVKLYDVFEDDDKLYLVMEYCEG-GDLFDLLKKRGLSEDEARFYARQILSALEY 113
QY 158 CHNCGVLHRDKDENILIDLNRGELKLDIFGSGALLKD--TVYTDPGTRVYSPPPWIRY 215
Db 114 LHSQGIHRLDKPENILLD-SDGHVKLADFLGAKQLDSGTLTTTFVGTPEYMAPE-VLL 171
QY 216 HRYHGRSAAWSGLILYDMVCGDIPFEHDEEILIRQVFRQ-----RVSSSE 262
Db 172 KGKYGKAVDWSGLVILYELLTKGPPFGDDQLL---ALFKKIGKPPPPPPPEWKISPE 228
QY 263 COHLIRWCLALRPSDRPTFEEIQNHWP 289
Db 229 AKDLIKKLVKDPKRLTAEALEHPF 255

RESULT 8

US-11-087-099-11500
; Sequence 11500, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11500
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-11-087-099-11500

Query Match 21.3%; Score 356; DB 7; Length 514;
Best Local Similarity 33.2%; Pred. No. 1.3e-24;
Matches 87; Conservative 54; Mismatches 105; Indels 16; Gaps 8;

QY 38 YQVGPLLAGSGFGSVYSGIRVSDNLPVAIKHVKDKRISDWGELPNGTRVPMEVVLLKKVYS 97
Db 19 YKLGKTLGIGSGFKVKIAEHTLTGHKVAVKILNRKRIRN---MDMEKVSREIKILRLPM 75
QY 98 SGFSGVIRLLDMFERPDSFVLILRPEPVQDLDFDITERGALQOEELARSFFQVLEAVRH 157
Db 76 --HPIHRLYEVIETPDSIYVVMYVKS-GELFDYIVEKGRLOEDEARNFFQOIISGVEY 132
QY 158 CHNCGVLHRDKDENILIDLNRGELKLDIFGSGALLKDTVYTFD-GTRVYSPPEWIRYH 216
Db 133 CHRNVMVHRDLKPENILLD-SKNVVKIADFGLSNIMRDGHFLKTCGSPNYAAPEVISGK 191
QY 217 RYHGRSAAWSGLILYDMVCGDIPFEHDEEIT-----IRGQVF-FRQVSECOHLIRW 269
Db 192 LYAGEVDVWVGVLVYALLCGTLFPD-DENIPNLFKKIKGGIYTLPSHLSAGARDLIPR 250
QY 270 CLALRPSDRPTFEEIQNHWP 291
Db 251 MLIVDPMKRWMTIPEIRLHPWFQ 272

RESULT 9

US-11-087-099-3997
; Sequence 3997, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3997
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-11-087-099-3997

Query Match 21.1%; Score 352; DB 7; Length 512;
Best Local Similarity 32.2%; Pred. No. 3.1e-24;
Matches 84; Conservative 55; Mismatches 108; Indels 14; Gaps 6;

QY 38 YQVGPLLAGSGFGSVYSGIRVSDNLPVAIKHVKDKRISDWGELPNGTRVPMEVVLLKKVYS 97
Db 19 YKLGKTLGIGSGFKVKIAEHTLTGHKVAVKILNRKRIRN---MDMEKVSREIKILRLPM 75
QY 98 SGFSGVIRLLDMFERPDSFVLILRPEPVQDLDFDITERGALQOEELARSFFQVLEAVRH 157
Db 76 HGH--ISRLYEVIETPDSIYVVMYVKS-GELFDYIVEKGRLOEDEARNFFQOIISGVEY 132

Qy	158	CHNCGVLRHDKDENILDLNRGEKLIDFGSGALLKOTVTYDFD-GTRVYSPPEWIRWH	216
Db	133	CHINMVAHRDLKPENLLLD-SKNWNKIADFGLSNNRDLGHFLTKTSCGSPNYAAPEVISGK	191
Qy	217	RHGSAAVMSLIGLTYDMVCGDIIPFHD-----EEIRGVFFQRVRSSCOHLIRWC	270
Db	192	LYAGPEVDVMVGCVIYALLCGLTFPFDDEINPLFKKIKGGYITLPShLSAGARDLIPRM	251
Qy*	271	LALRPDRPTFEETQNHPMQ	291
Db	252	LIVDPMKMTIPEIRLHPWFQ	272

```

RESULT 10
US-11-087-099-3612
; Sequence 3612, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3612
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-11-087-099-3612

```

Query Match	21.1%	Score 352;	DB 7;	Length 514;
Best Local Similarity	32.2%	Pred. No. 3.le-24;		
Matches	84;	Conservative 55;	Mismatches 108;	Indels 14; Gaps 6;
Qy	38	QYQCPLGSGCGSVSGIRVSDNLVPAIKHVEKDRISDWGELPNGTVPMPVEVLLKKVS	97	
Db	19	YKLGKTTIGISGFKVKVTAETHLIGHKVAVKVILNRRKRN--MDMEEKVSBEIKILRFM	75	
Qy	98	SGRSGVRLLLDWFRRPDSFVLLILRPEPVQDLDFDITERGALQBELARSFPOVLEAVRH	157	
Db	76	HGH--ISRLYEVIPTPSDIYVMVYKVS-GLSFYIIVEKQLQDEARNFQQIISGVEY	132	
Qy	158	CHNCGVLHRTDKENILIDLNRGELKILDFGSGALLKDTVYTFD-GRVTVSPPEWIRYH	216	
Db	133	CHINWVHRDLKPNLLLD-SKNVVKTADFGLSNIMRDGHFLKTCGSPNVAAPEVTSKG	191	
Qy	217	RYHGRSAAVSGILLYDMVCGDIPFEHD-----EEIRIQVFPFRQVSSCEQHILNRC	270	
Db	192	LYAGPEVDVMSGVILYALLCGTLFPDDDENIPNLFKKIKGGVITLPSHLSAGADLIPRM	251	
Qy	271	LALRPSDRPTEETONHPWQ	291	
Db	252	LIVDPMKRMTIPEIRLHPWFO	272	

```

RESULT 11
US-11-087-099-12402
; Sequence 12402, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12402
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Candida tropicalis
US-11-087-099-12402

```

Query Match 20.9%; Score 348.5; DB 7; Length 619;

[illegible]

```

RESULT 12
US-11-087-099-11838
; Sequence 11838, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11838
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Guillardia theta
US-11-087-099-11838

```

Query Match	20.8%;	Score 348;	DB 7;	Length 472;
Best Local Similarity	32.3%;	Pred. No. 6.4e-24;		
Matches	92;	Conservative 49;	Mismatches 118;	Indels 26; Gaps 9;
Qy	18	NDLHATKLAPCKEKEPLESQQVCPILGSGGPGSVYSGIRVSDNLPVAIKHVEKDRISDW	77	
Db	2	NKLFSIKIGP-----YYLGKTLGVSGFGVKLGEHCLGQKQVAVKILNRKKTKN-	50	
Qy	78	GELPNGTRVPMVEVVLKKYVSSGFGVIRLLDWERPDSFVLLERPEPVODLDFITERG	137	
Db	51	--LQMEKVKREICILKFM--HPHILRLYEVIETPTDIFVVTYITG-GELFPDYIVERG	105	
Qy	138	ALQBELARSFFWOVLAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKQTV	197	
Db	106	RLNEDSRKEFPQMGISGIEYCHNNVVRDLKKNLILLDAHL-NVKIADFGLSNIMKQGN	164	
Qy	198	YTFDPD-GTRYVSPPEIRYHRHGRSAAVWSGLILYDMVCGDIPPEHDEEI-----IR	250	
Db	165	FLKTS CGSPNYAAPEVINGSKYLGPVDVWSCGVIMYALLCGSLPFD-DENIPNLKKIK	223	
Qy	251	GOVFFRQRVSSE-CQHLIRWCIALRSDRPTTFEEIQNHPPMQDVL	294	
Db	224	SGVILPGLVSLDSRDMIAQMLITNPLRTTINEIRDPHFNSRL	268	

RESULT 13
US-10-770-726-67
; Sequence 67, Application US/10770726
; Publication No. US2005026409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene

```
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-67

Query Match      20.5%; Score 342.5; DB 6; Length 651;
Best Local Similarity 33.2%; Pred. No. 3.1e-23;
Matches 97; Conservative 51; Mismatches 117; Indels 27; Gaps 10;

QY 29 KEKEPLESOYQVGPLLGSGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPM 88
Db 2 KOYDELLKYYELHETIGTGFAKVKLACHILTGEMVAIKIMDKNTLG--SDLP---RIKT 56

QY 89 EVVLLKKVSGSGVIRLDDWFERPDSFVLIILERPEFVQDLDFITERGALQOEELARSFF 148
Db 57 EIEALKNLR--HQHICQLYHVLETANKIFMWLEYC--PGGELFDYIISQDRLSEETRVVF 113

QY 149 MQVLEAVRHCHNGVLRHDIKDENILIDLNRGELKLIIDFGSGALLKDTVYTFD-----G 203
Db 114 RQIVSAVAVYVHSGQVAHRDLKPENLLFD--EYHKLKLIIDFGCAKPKGN--KDYHLQTCG 170

QY 204 TRVYSPPEWIRYHRHGRSAAVWSLIGILLYDMVCGDIPFEHD-----BEIRGQVFFRQ 257
Db 171 SLAYAAPELIQKSYLGSEADVWSMGILLYVLMCGFLPDDDDNNMALYKKIMRGKYDVPK 230

QY 258 RVSSQCHLIRWCLALRPSDRPTFEEIQNHWP--MQDVLLPQETAE-----IHL 304
Db 231 WLSPPSILLQQMLQVDPKKRISMKNLNHPWIMQDYNYPVWQSKNPFHIL 282

US-11-177-138-10

Query Match      20.5%; Score 342.5; DB 7; Length 651;
Best Local Similarity 33.2%; Pred. No. 3.1e-23;
Matches 97; Conservative 51; Mismatches 117; Indels 27; Gaps 10;

QY 29 KEKEPLESOYQVGPLLGSGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPM 88
Db 2 KOYDELLKYYELHETIGTGFAKVKLACHILTGEMVAIKIMDKNTLG--SDLP---RIKT 56

QY 89 EVVLLKKVSGSGVIRLDDWFERPDSFVLIILERPEFVQDLDFITERGALQOEELARSFF 148
Db 57 EIEALKNLR--HQHICQLYHVLETANKIFMWLEYC--PGGELFDYIISQDRLSEETRVVF 113

QY 149 MQVLEAVRHCHNGVLRHDIKDENILIDLNRGELKLIIDFGSGALLKDTVYTFD-----G 203
Db 114 RQIVSAVAVYVHSGQVAHRDLKPENLLFD--EYHKLKLIIDFGCAKPKGN--KDYHLQTCG 170

QY 204 TRVYSPPEWIRYHRHGRSAAVWSLIGILLYDMVCGDIPFEHD-----BEIRGQVFFRQ 257
Db 171 SLAYAAPELIQKSYLGSEADVWSMGILLYVLMCGFLPDDDDNNMALYKKIMRGKYDVPK 230

QY 258 RVSSQCHLIRWCLALRPSDRPTFEEIQNHWP--MQDVLLPQETAE-----IHL 304
Db 231 WLSPPSILLQQMLQVDPKKRISMKNLNHPWIMQDYNYPVWQSKNPFHIL 282

US-11-177-138-10

Query Match      20.5%; Score 342.5; DB 7; Length 651;
Best Local Similarity 33.2%; Pred. No. 3.1e-23;
Matches 97; Conservative 51; Mismatches 117; Indels 27; Gaps 10;

QY 29 KEKEPLESOYQVGPLLGSGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPM 88
Db 2 KOYDELLKYYELHETIGTGFAKVKLACHILTGEMVAIKIMDKNTLG--SDLP---RIKT 56

QY 89 EVVLLKKVSGSGVIRLDDWFERPDSFVLIILERPEFVQDLDFITERGALQOEELARSFF 148
Db 57 EIEALKNLR--HQHICQLYHVLETANKIFMWLEYC--PGGELFDYIISQDRLSEETRVVF 113
```

```
QY 149 MQVLEAVRHCHNGVLRHDIKDENILIDLNRGELKLIIDFGSGALLKDTVYTFD-----G 203
Db 114 RQIVSAVAVYVHSGQVAHRDLKPENLLFD--EYHKLKLIIDFGCAKPKGN--KDYHLQTCG 170
QY 204 TRVYSPPEWIRYHRHGRSAAVWSLIGILLYDMVCGDIPFEHD-----BEIRGQVFFRQ 257
Db 171 SLAYAAPELIQKSYLGSEADVWSMGILLYVLMCGFLPDDDDNNMALYKKIMRGKYDVPK 230
QY 258 RVSSQCHLIRWCLALRPSDRPTFEEIQNHWP--MQDVLLPQETAE-----IHL 304
Db 231 WLSPPSILLQQMLQVDPKKRISMKNLNHPWIMQDYNYPVWQSKNPFHIL 282
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RESULT 15
US-11-096-568A-22124
; Sequence 22124, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22124
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(464)
; OTHER INFORMATION: Ceres Seq. ID no. 12407640
US-11-096-568A-22124
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Query Match      20.5%; Score 342; DB 7; Length 464;
Best Local Similarity 30.9%; Pred. No. 2.2e-23;
Matches 93; Conservative 48; Mismatches 112; Indels 48; Gaps 7;
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QY 28 GKEKEPLESQ-----YQVGPLLGSGFGSVY-----SGIRVSDNLPVAIKHVEKORI 74
Db 5 GREAEFGEEERKLVGLKVELGRLLGQGTFAKYYVARDLSAGAGTGHSCSVAIKVIDKARL 64

QY 75 SDWGELPNGTRVPM-----EVLKKVSSGSGVIRLDDWFERPDSFVLIILERPFP 125
Db 65 RTEGMEQLEKREISIMRMVRHPNVGVIREVLASRSRVFVVMYARGGELFAKV----- 118

QY 126 VQDLDFITERGALQOEELARSFFMQVLEAVRHCHNGVLRHDIKDENILIDLNRGELKLI 185
Db 119 -----ARGLDEDHARRYFQQLVAAGVCHRRGVAHRDLKPENLLD--EAGELKVT 168

QY 186 DFGSGALLK-----DTVYTFDQTRVYSPPEWIRYHRHGRSAAVWSLIGILLYDMVCGDIP 241
Db 169 DFLAALPEQLRHDGLLHTQCGTPAYVAPEVLKRGYDGGARADLWSCGVLYVLLCGFLP 228

QY 242 FEHDEIRGQVFFRQR-----VSSEQHLIRWCLALRPSDRPTFEEIQNHWPWQDVLL 295
Db 229 FQHDNYVLYQKIFKADYQVPPVWVSGDARRLLIARLLVWDPKARASTAEINCTPWFKGFV 288

QY 296 P 296
Db 289 P 289
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Search completed: April 21, 2006, 13:14:14
Job time : 27 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2006, 13:10:04 ; Search time 166 Seconds
(without alignments)
787.835 Million cell updates/sec

Title: US-10-664-421-1
Perfect score: 1670
Sequence: 1 MLLSKINSLAHURAAPCNDL.....LLPQETABIHLHLSLSPGFSK 313

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /cgn2_6/protdata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/protdata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/protdata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/protdata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/protdata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/protdata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1670	100.0	313	3	US-09-971-791-9
2	1670	100.0	313	4	US-10-081-113-18
3	1670	100.0	313	4	US-10-394-322A-52
4	1670	100.0	313	4	US-10-348-081-13
5	1670	100.0	313	4	US-10-664-421-1
6	1670	100.0	313	4	US-10-664-421-150
7	1670	100.0	313	4	US-10-705-757-2
8	1670	100.0	313	4	US-10-377-268-9
9	1670	100.0	313	5	US-10-951-389-18
10	1670	100.0	313	5	US-10-951-406-18
11	1670	100.0	313	5	US-10-951-477-18
12	1670	100.0	313	5	US-10-977-087-18
13	1670	100.0	313	5	US-10-941-635-1
14	1670	100.0	313	5	US-10-941-635-152
15	1657	99.2	313	4	US-10-620-052A-22
16	1636	98.0	313	3	US-09-971-791-8
17	1636	98.0	313	4	US-10-348-081-12
18	1636	98.0	313	4	US-10-705-757-4
19	1582	94.7	313	3	US-09-971-791-7
20	1582	94.7	313	4	US-10-348-081-14
21	1582	94.7	313	4	US-10-664-421-2
22	1582	94.7	313	4	US-10-705-757-6
23	1582	94.7	313	4	US-10-377-268-10
24	1582	94.7	313	5	US-10-941-635-2
25	1362	81.6	253	4	US-10-620-052A-71
26	1140	68.3	323	4	US-10-664-421-7
27	1140	68.3	323	4	US-10-377-268-15

28	1140	68.3	323	5	US-10-941-635-7	Sequence 7, Appli
29	1135	68.0	374	4	US-10-425-114-54275	Sequence 54275, A
30	1133	67.8	326	3	US-09-971-791-2	Sequence 2, Appli
31	1133	67.8	326	4	US-10-348-081-2	Sequence 2, Appli
32	1133	67.8	326	4	US-10-664-421-166	Sequence 166, App
33	1133	67.8	326	4	US-10-618-941-82	Sequence 82, Appli
34	1133	67.8	374	4	US-10-425-114-54264	Sequence 54264, A
35	1129.5	67.6	326	4	US-10-348-081-6	Sequence 6, Appli
36	1129.5	67.6	326	4	US-10-705-757-11	Sequence 11, Appli
37	1129.5	67.6	326	4	US-10-377-268-14	Sequence 14, Appli
38	1129.5	67.6	326	5	US-10-941-635-6	Sequence 6, Appli
39	1128.5	67.6	326	4	US-10-348-081-10	Sequence 10, Appli
40	1128.5	67.6	326	4	US-10-705-757-9	Sequence 9, Appli
41	1128.5	67.6	455	3	US-09-971-791-5	Sequence 5, Appli
42	1116	66.8	325	4	US-10-664-421-6	Sequence 6, Appli
43	1105	66.2	323	3	US-09-971-791-6	Sequence 6, Appli
44	1105	66.2	323	4	US-10-348-081-11	Sequence 11, Appli
45	1105	66.2	323	4	US-10-664-421-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-971-791-9
; Sequence 9, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle MacBeth
; FILE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971,791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-791-9

Query Match	100.0%;	Score 1670;	DB 3;	Length 313;
Best Local Similarity	100.0%;	Pred. No. 2.2e-143;		
Matches 313;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MLLSKINSLAHURAAPCNDLHATKLPAGEKEPLESQYQVGLGSGGFGSVYSGIRVSD	60	
Db	1	MLLSKINSLAHURAAPCNDLHATKLPAGEKEPLESQYQVGLGSGGFGSVYSGIRVSD	60	
QY	61	NLPVAIKHVKEDRIISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLLI	120	
Db	61	NLPVAIKHVKEDRIISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLLI	120	
QY	121	ERPEVPQDLFFITRGALQBELARSPFWQVLEAVRHCHNCVGLHRDKDENILIDLNRG	180	
Db	121	ERPEVPQDLFFITRGALQBELARSPFWQVLEAVRHCHNCVGLHRDKDENILIDLNRG	180	
QY	181	EKLIDFGSGALLKDTVTDFDGTAVYPPPEWIRVHYHGRSAAVWSGLILLYDMVCGDI	240	
Db	181	EKLIDFGSGALLKDTVTDFDGTAVYPPPEWIRVHYHGRSAAVWSGLILLYDMVCGDI	240	
QY	241	PFHEDEIIRGQVFFRQVRSSECCQLINWCLALRPSDRPTTFEEIQNHPPMQDVLPLQETA	300	
Db	241	PFHEDEIIRGQVFFRQVRSSECCQLINWCLALRPSDRPTTFEEIQNHPPMQDVLPLQETA	300	
QY	301	EHLHLSLSPGFSK	313	


```
Db 301 EIHLSLSPGSK 313

RESULT 2
US-10-081-119-18
; Sequence 18, Application US/10081119
; Publication No. US20030045491A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/081,119
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-081-119-18

Query Match 100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEKEPLESOYQVGPLLGSGGFGSVYSGIRVSD 60
Db 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEKEPLESOYQVGPLLGSGGFGSVYSGIRVSD 60
Qy 61 NLPVAIKHVEKDRISDMGELPENGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
Db 61 NLPVAIKHVEKDRISDMGELPENGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
Qy 121 ERPEPVQDLFDFTTERGALQBELARSPFWQVLEAVRHCHNCVGLHRDIKDNILIDLNRG 180
Db 121 ERPEPVQDLFDFTTERGALQBELARSPFWQVLEAVRHCHNCVGLHRDIKDNILIDLNRG 180
Qy 181 ELKLIDFGSGALLKDTVTYDFDGTFRVYSPPEWIRVHRVHGRSAAVWSLGLILLYDMVCGDI 240
Db 181 ELKLIDFGSGALLKDTVTYDFDGTFRVYSPPEWIRVHRVHGRSAAVWSLGLILLYDMVCGDI 240
Qy 241 PFEHDEEIIIRGOVFFRQVRSSECOHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPPQETA 300
Db 241 PFEHDEEIIIRGOVFFRQVRSSECOHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPPQETA 300
Qy 301 EIHLSLSPGSK 313
Db 301 EIHLSLSPGSK 313

RESULT 4
US-10-348-081-13
; Sequence 13, Application US/10348081
; Publication No. US20040038246A1
; GENERAL INFORMATION:
; APPLICANT: KORN, Marcus
; APPLICANT: MUELLER, Guenter
; APPLICANT: SCHNEIDER, Rudolf
; APPLICANT: TSCHANK, Georg
; TITLE OF INVENTION: PTM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
; FILE REFERENCE: DEAV2002/0004 US NP
; CURRENT APPLICATION NUMBER: US/10/348,081
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-081-13

Query Match 100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEKEPLESOYQVGPLLGSGGFGSVYSGIRVSD 60
Db 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEKEPLESOYQVGPLLGSGGFGSVYSGIRVSD 60
Qy 61 NLPVAIKHVEKDRISDMGELPENGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
Db 61 NLPVAIKHVEKDRISDMGELPENGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
Qy 121 ERPEPVQDLFDFTTERGALQBELARSPFWQVLEAVRHCHNCVGLHRDIKDNILIDLNRG 180
Db 121 ERPEPVQDLFDFTTERGALQBELARSPFWQVLEAVRHCHNCVGLHRDIKDNILIDLNRG 180
Qy 181 ELKLIDFGSGALLKDTVTYDFDGTFRVYSPPEWIRVHRVHGRSAAVWSLGLILLYDMVCGDI 240
Db 181 ELKLIDFGSGALLKDTVTYDFDGTFRVYSPPEWIRVHRVHGRSAAVWSLGLILLYDMVCGDI 240

Db 301 EIHLSLSPGSK 313
301 EIHLSLSPGSK 313

RESULT 3
US-10-394-322A-52
; Sequence 52, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; *APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 70
; SEQ ID NO 52
; LENGTH: 313
; TYPE: PRT
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QY 241 PPEHDEIIRGOVFRQVRVSSCQHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPPQETA 300
Db 241 PPEHDEIIRGOVFRQVRVSSCQHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPPQETA 300
QY 301 EIHLSLSPGSK 313
Db 301 EIHLSLSPGSK 313

RESULT 5

US-10-664-421-1
; Sequence 1, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-1

Query Match 100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.2e-143; Mismatches 0; Indels 0; Gaps 0;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLSKINSIAHLRAAPCNDLHATKAPGKEPLESQVQVGLGSGFGSVYSGIRVSD 60
Db 1 MLLSKINSIAHLRAAPCNDLHATKAPGKEPLESQVQVGLGSGFGSVYSGIRVSD 60
QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
Db 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
QY 121 ERPEPVQDLFDITFERGALQEBELARSPFWQVLEAVRHCHNCVGLHRDKDENILIDLNRG 180
Db 121 ERPEPVQDLFDITFERGALQEBELARSPFWQVLEAVRHCHNCVGLHRDKDENILIDLNRG 180
QY 181 ELKLIDFGSGALLKDTVTYDFDGTIRVYSPPEWIRYHRYHGRSAAVWSLGLLYDMVCGDI 240
Db 181 ELKLIDFGSGALLKDTVTYDFDGTIRVYSPPEWIRYHRYHGRSAAVWSLGLLYDMVCGDI 240
QY 241 PPEHDEIIRGOVFRQVRVSSCQHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPPQETA 300
Db 241 PPEHDEIIRGOVFRQVRVSSCQHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPPQETA 300
QY 301 EIHLSLSPGSK 313
Db 301 EIHLSLSPGSK 313

RESULT 6

US-10-664-421-150
; Sequence 150, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN

; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 150
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-150

Query Match 100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.2e-143; Mismatches 0; Indels 0; Gaps 0;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLSKINSIAHLRAAPCNDLHATKAPGKEPLESQVQVGLGSGFGSVYSGIRVSD 60
Db 1 MLLSKINSIAHLRAAPCNDLHATKAPGKEPLESQVQVGLGSGFGSVYSGIRVSD 60
QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
Db 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
QY 121 ERPEPVQDLFDITFERGALQEBELARSPFWQVLEAVRHCHNCVGLHRDKDENILIDLNRG 180
Db 121 ERPEPVQDLFDITFERGALQEBELARSPFWQVLEAVRHCHNCVGLHRDKDENILIDLNRG 180
QY 181 ELKLIDFGSGALLKDTVTYDFDGTIRVYSPPEWIRYHRYHGRSAAVWSLGLLYDMVCGDI 240
Db 181 ELKLIDFGSGALLKDTVTYDFDGTIRVYSPPEWIRYHRYHGRSAAVWSLGLLYDMVCGDI 240
QY 241 PPEHDEIIRGOVFRQVRVSSCQHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPPQETA 300
Db 241 PPEHDEIIRGOVFRQVRVSSCQHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPPQETA 300
QY 301 EIHLSLSPGSK 313
Db 301 EIHLSLSPGSK 313

RESULT 7

US-10-705-757-2
; Sequence 2, Application US/10705757
; Publication No. US20040146942A1
; GENERAL INFORMATION:
; APPLICANT: GRUENENTHAL GMBH
; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
; FILE REFERENCE: 029310.52818US
; CURRENT APPLICATION NUMBER: US/10/705,757
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/EP02/05234
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: DE 101 23 055.9
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-757-2

Query Match 100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.2e-143; Mismatches 0; Indels 0; Gaps 0;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLSKINSIAHLRAAPCNDLHATKAPGKEPLESQVQVGLGSGFGSVYSGIRVSD 60

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Db      |||||||
1 MLLSKINSLAHLRAAPCNDLHATKAPGKEKEPLESQVQVGLLGGSGFGSGYSGIRVSD 60
Qy      |||||||
61 NLPVAIKHVEKDRISDWGELNGTRVPMVEVLLKKVSSGFGSVIRLLDWFPERPDSFVLIL 120
Db      |||||||
61 NLPVAIKHVEKDRISDWGELNGTRVPMVEVLLKKVSSGFGSVIRLLDWFPERPDSFVLIL 120
Qy      |||||||
121 ERPEVQDLFDFTTERGALQELARSAFFWQVLEAVRHCHNCVGLHRDICKDENILIDLNRG 180
Db      |||||||
121 ERPEVQDLFDFTTERGALQELARSAFFWQVLEAVRHCHNCVGLHRDICKDENILIDLNRG 180
Qy      |||||||
181 ELKLIDFGSGALLKDTVTYDFDGTTRVYSPPEWIRYHRVHGRSAVAWSLGLILLYDMVCGDI 240
Db      |||||||
181 ELKLIDFGSGALLKDTVTYDFDGTTRVYSPPEWIRYHRVHGRSAVAWSLGLILLYDMVCGDI 240
Qy      |||||||
241 PFEHDEEIIIRQVFFRQVRSSECQHLIRWCLALRPSDRPTFEEIQNHHPMODVLLPQETA 300
Db      |||||||
241 PFEHDEEIIIRQVFFRQVRSSECQHLIRWCLALRPSDRPTFEEIQNHHPMODVLLPQETA 300
Qy      |||||||
301 EIHLSLSPGSPK 313
Db      |||||||
301 EIHLSLSPGSPK 313
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RESULT 8

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US-10-377-268-9
; Sequence 9, Application US/10377268
; Publication No. US20040171062A1
; GENERAL INFORMATION:
; APPLICANT: HIRTH, KLAUS-PRTER
; APPLICANT: MILBURN, MICHAEL VANCE
; TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
; FILE REFERENCE: 039363/0303
; CURRENT APPLICATION NUMBER: US/10/377,268
; PRIOR FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2003-01-02
; PRIOR FILING DATE: 2003-01-02
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-04-12,341
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-377-268-9
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Query Match      100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLLSKINSLAHLRAAPCNDLHATKAPGKEKEPLESQVQVGLLGGSGFGSGYSGIRVSD 60
Db      1 MLLSKINSLAHLRAAPCNDLHATKAPGKEKEPLESQVQVGLLGGSGFGSGYSGIRVSD 60
Qy      61 NLPVAIKHVEKDRISDWGELNGTRVPMVEVLLKKVSSGFGSVIRLLDWFPERPDSFVLIL 120
Db      61 NLPVAIKHVEKDRISDWGELNGTRVPMVEVLLKKVSSGFGSVIRLLDWFPERPDSFVLIL 120
Qy      121 ERPEVQDLFDFTTERGALQELARSAFFWQVLEAVRHCHNCVGLHRDICKDENILIDLNRG 180
Db      121 ERPEVQDLFDFTTERGALQELARSAFFWQVLEAVRHCHNCVGLHRDICKDENILIDLNRG 180
Qy      181 ELKLIDFGSGALLKDTVTYDFDGTTRVYSPPEWIRYHRVHGRSAVAWSLGLILLYDMVCGDI 240
Db      181 ELKLIDFGSGALLKDTVTYDFDGTTRVYSPPEWIRYHRVHGRSAVAWSLGLILLYDMVCGDI 240
Qy      241 PFEHDEEIIIRQVFFRQVRSSECQHLIRWCLALRPSDRPTFEEIQNHHPMODVLLPQETA 300
Db      241 PFEHDEEIIIRQVFFRQVRSSECQHLIRWCLALRPSDRPTFEEIQNHHPMODVLLPQETA 300
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Db      241 PFEHDEEIIIRQVFFRQVRSSECQHLIRWCLALRPSDRPTFEEIQNHHPMODVLLPQETA 300
Qy      301 EIHLSLSPGSPK 313
Db      301 EIHLSLSPGSPK 313

RESULT 9
US-10-951-389-18
; Sequence 18, Application US/10951389
; Publication No. US20050058627A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in diagnosis and as a Therapeutic
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,389
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-389-18
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Query Match      100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLLSKINSLAHLRAAPCNDLHATKAPGKEKEPLESQVQVGLLGGSGFGSGYSGIRVSD 60
Db      1 MLLSKINSLAHLRAAPCNDLHATKAPGKEKEPLESQVQVGLLGGSGFGSGYSGIRVSD 60
Qy      61 NLPVAIKHVEKDRISDWGELNGTRVPMVEVLLKKVSSGFGSVIRLLDWFPERPDSFVLIL 120
Db      61 NLPVAIKHVEKDRISDWGELNGTRVPMVEVLLKKVSSGFGSVIRLLDWFPERPDSFVLIL 120
Qy      121 ERPEVQDLFDFTTERGALQELARSAFFWQVLEAVRHCHNCVGLHRDICKDENILIDLNRG 180
Db      121 ERPEVQDLFDFTTERGALQELARSAFFWQVLEAVRHCHNCVGLHRDICKDENILIDLNRG 180
Qy      181 ELKLIDFGSGALLKDTVTYDFDGTTRVYSPPEWIRYHRVHGRSAVAWSLGLILLYDMVCGDI 240
Db      181 ELKLIDFGSGALLKDTVTYDFDGTTRVYSPPEWIRYHRVHGRSAVAWSLGLILLYDMVCGDI 240
Qy      241 PFEHDEEIIIRQVFFRQVRSSECQHLIRWCLALRPSDRPTFEEIQNHHPMODVLLPQETA 300
Db      241 PFEHDEEIIIRQVFFRQVRSSECQHLIRWCLALRPSDRPTFEEIQNHHPMODVLLPQETA 300
Qy      301 EIHLSLSPGSPK 313
Db      301 EIHLSLSPGSPK 313
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RESULT 10

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US-10-951-406-18
; Sequence 18, Application US/10951406
; Publication No. US20050059630A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in diagnosis and as a Therapeutic
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,406
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; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-477-18

Query Match      100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQVQVGLLGGGFGSVYSGIRVSD 60
Db 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQVQVGLLGGGFGSVYSGIRVSD 60
QY 61 NLPVAIKHVKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFEPDPSFVLIL 120
Db 61 NLPVAIKHVKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFEPDPSFVLIL 120
QY 121 ERPEVQDLFDFTTGERGALQBELARSPFWQVLEAVRHCHNCGLVLRDIDKDNILIDLNRG 180
Db 121 ERPEVQDLFDFTTGERGALQBELARSPFWQVLEAVRHCHNCGLVLRDIDKDNILIDLNRG 180
QY 181 ELKLIDFGSGALLKDTVTYDFDGTTRVYSPPEWIRVHRVHGRSAAVWSLGLLYDMVCGDI 240
Db 181 ELKLIDFGSGALLKDTVTYDFDGTTRVYSPPEWIRVHRVHGRSAAVWSLGLLYDMVCGDI 240
QY 241 PFEHDEEIRGQVFRQVRVSSCOHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPLQETA 300
Db 241 PFEHDEEIRGQVFRQVRVSSCOHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPLQETA 300
QY 301 EIHLSLSPGPSK 313
Db 301 EIHLSLSPGPSK 313

RESULT 12
US-10-977-087-18
; Sequence 18, Application US/10977087
; Publication No. US20050130926A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; APPLICANT: Kaufmann, Joerg
; APPLICANT: Xin, Hong
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Khoja, Hamiduddin
; APPLICANT: Shyamala, Venkatakrishna
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS CELLS
; FILE REFERENCE: 2300-21986
; CURRENT APPLICATION NUMBER: US/10/977,087
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: 10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/271,254
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 10/360,848
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: 09/570,593
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,112
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 10/763,692
; PRIOR FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: 09/626,301
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/148,936
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/145,612
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 10/698,959
; PRIOR FILING DATE: 2003-10-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-977-087-18

Query Match      100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQVQVGLLGGGFGSVYSGIRVSD 60
Db 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQVQVGLLGGGFGSVYSGIRVSD 60
QY 61 NLPVAIKHVKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFEPDPSFVLIL 120
Db 61 NLPVAIKHVKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFEPDPSFVLIL 120
QY 121 ERPEVQDLFDFTTGERGALQBELARSPFWQVLEAVRHCHNCGLVLRDIDKDNILIDLNRG 180
Db 121 ERPEVQDLFDFTTGERGALQBELARSPFWQVLEAVRHCHNCGLVLRDIDKDNILIDLNRG 180
QY 181 ELKLIDFGSGALLKDTVTYDFDGTTRVYSPPEWIRVHRVHGRSAAVWSLGLLYDMVCGDI 240
Db 181 ELKLIDFGSGALLKDTVTYDFDGTTRVYSPPEWIRVHRVHGRSAAVWSLGLLYDMVCGDI 240
QY 241 PFEHDEEIRGQVFRQVRVSSCOHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPLQETA 300
Db 241 PFEHDEEIRGQVFRQVRVSSCOHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPLQETA 300
QY 301 EIHLSLSPGPSK 313
Db 301 EIHLSLSPGPSK 313

RESULT 11
US-10-951-477-18
; Sequence 18, Application US/10951477
; Publication No. US20050063974A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,477
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-477-18

Query Match      100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQVQVGLLGGGFGSVYSGIRVSD 60
Db 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQVQVGLLGGGFGSVYSGIRVSD 60
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QY 1 MLLSKINSLAHLRAAPCNDLHATKLPCKEKEPLESQVQVGLGSGFGSVYSGIRVSD 60
DB 1 MLLSKINSLAHLRAAPCNDLHATKLPCKEKEPLESQVQVGLGSGFGSVYSGIRVSD 60
QY 61 NLPVAIKHVEKDRISDMGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
DB 61 NLPVAIKHVEKDRISDMGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
QY 121 ERPEPVQDLFDITERGALQBELARSPFWQVLEAVRHCHNCGVLRHDIKDENILIDLNRG 180
DB 121 ERPEPVQDLFDITERGALQBELARSPFWQVLEAVRHCHNCGVLRHDIKDENILIDLNRG 180
QY 181 ELKLIDFGSGALLKDTVTYDFDGRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240
DB 181 ELKLIDFGSGALLKDTVTYDFDGRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240
QY 241 PFEHDEEIIIRQVFRQVRVSSECOHLIRWCLALRPSDRPTPEEIQNHHPWMDVLLPQETA 300
DB 241 PFEHDEEIIIRQVFRQVRVSSECOHLIRWCLALRPSDRPTPEEIQNHHPWMDVLLPQETA 300
QY 301 EIHLSLSPGSPK 313
DB 301 EIHLSLSPGSPK 313

RESULT 13

US-10-941-635-1
; Sequence 1, Application US/10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-941-635-1

Query Match 100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MLLSKINSLAHLRAAPCNDLHATKLPCKEKEPLESQVQVGLGSGFGSVYSGIRVSD 60
QY 61 NLPVAIKHVEKDRISDMGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
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QY 121 ERPEPVQDLFDITERGALQBELARSPFWQVLEAVRHCHNCGVLRHDIKDENILIDLNRG 180
DB 121 ERPEPVQDLFDITERGALQBELARSPFWQVLEAVRHCHNCGVLRHDIKDENILIDLNRG 180
QY 181 ELKLIDFGSGALLKDTVTYDFDGRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240
DB 181 ELKLIDFGSGALLKDTVTYDFDGRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240
QY 241 PFEHDEEIIIRQVFRQVRVSSECOHLIRWCLALRPSDRPTPEEIQNHHPWMDVLLPQETA 300

DB 241 PFEHDEEIIIRQVFRQVRVSSECOHLIRWCLALRPSDRPTPEEIQNHHPWMDVLLPQETA 300
QY 301 EIHLSLSPGSPK 313
DB 301 EIHLSLSPGSPK 313

RESULT 14

US-10-941-635-152
; Sequence 152, Application US/10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 152
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
US-10-941-635-152

Query Match 100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 NLPVAIKHVEKDRISDMGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
QY 121 ERPEPVQDLFDITERGALQBELARSPFWQVLEAVRHCHNCGVLRHDIKDENILIDLNRG 180
DB 121 ERPEPVQDLFDITERGALQBELARSPFWQVLEAVRHCHNCGVLRHDIKDENILIDLNRG 180
QY 181 ELKLIDFGSGALLKDTVTYDFDGRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240
DB 181 ELKLIDFGSGALLKDTVTYDFDGRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240
QY 241 PFEHDEEIIIRQVFRQVRVSSECOHLIRWCLALRPSDRPTPEEIQNHHPWMDVLLPQETA 300
DB 241 PFEHDEEIIIRQVFRQVRVSSECOHLIRWCLALRPSDRPTPEEIQNHHPWMDVLLPQETA 300
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DB 301 EIHLSLSPGSPK 313

RESULT 15

US-10-620-052A-22
; Sequence 22, Application US/10620052A
; Publication No. US20040126784A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Markovtsov, Vadim
; APPLICANT: Rigel Pharmaceuticals, Inc.

; TITLE OF INVENTION: Modulators of Cellular Proliferation
; FILE REFERENCE: 021044-004010US
; CURRENT APPLICATION NUMBER: US/10/620,052A
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/395,443
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: PIM1 oncogene serine threonine kinase
US-10-620-052A-22

Query Match 99.2%; Score 1657; DB 4; Length 313;
Best Local Similarity 99.4%; Pred. No. 3.3e-142;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db	1	MLLSKINSIAHLRAACNDLHATKLPAGKEKPLESQYQVGPILLGSGGFGSVYSGIRVSD	60
QY	61	NLPVAIKHVEKDRISDWGELPNGTRVPMEVLLKKVSSGFGSGVIRLLDMFERPDSFVLIL	120
Db	61	NLPVAIKHVEKDRISDWGELPNGTRVPMEVLLKKVSSGFGSGVIRLLDMFERPDSFVLIL	120
QY	121	ERPEPVQDLFDITERGALQEELARSFFWQVLEAVHCHNCVGLHRDIKDENILIDLNRG	180
Db	121	ERPEPVQDLFDITERGALQEELARSFFWQVLEAVHCHNCVGLHRDIKDENILIDLNRG	180
QY	181	ELKLIDFGSGALLKDTVYTFDGTTRYSPPEWIRYHRYHGRSAAVMSLGILLYDMVCGDI	240
Db	181	ELKLIDFGSGALLKDTVYTFDGTTRYSPPEWIRYHRYHGRSAAVMSLGILLYDMVCGDI	240
QY	241	PFEHDEEIIIRGOVFFRQVSSSCOHLIRWCLALRPSDRPTFEEIQNHPPMQDVLQPETA	300
Db	241	PFEHDEEIIIRGOVFFRQVSSSCOHLIRWCLALRPSDRPTFEEIQNHPPMQDVLQPETA	300
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Db	301	EIHLHSLSPGSK	313

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Job time : 167 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2006, 12:58:49 ; Search time 47 Seconds
(without alignments)
550.585 Million cell updates/sec

Title: US-10-664-421-1
Perfect score: 1670
Sequence: 1 MLLSKINSLAHLRAAPCNDL.....LLPQETAIEHLHLSLSPGSPK 313

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/baCkfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1670	100.0	313	2	US-09-237-543-9
2	1670	100.0	313	2	US-09-644-450-9
3	1657	99.2	313	1	US-08-463-081B-26
4	1657	99.2	313	1	US-08-461-379A-26
5	1657	99.2	313	1	US-08-462-390B-26
6	1657	99.2	313	2	US-08-463-074B-26
7	1657	99.2	313	2	US-08-465-585C-26
8	1657	99.2	313	2	US-08-652-446-26
9	1636	98.0	313	2	US-09-237-543-8
10	1636	98.0	313	2	US-09-644-450-8
11	1582	94.7	313	2	US-09-237-543-7
12	1582	94.7	313	2	US-09-644-450-7
13	1296.5	77.6	257	1	US-07-857-224B-41
14	1133	67.8	326	2	US-09-237-543-2
15	1133	67.8	326	2	US-09-644-450-2
16	1128.5	67.6	455	2	US-09-237-543-5
17	1128.5	67.6	455	2	US-09-644-450-5
18	1105	66.2	323	2	US-09-237-543-6
19	1105	66.2	323	2	US-09-644-450-6
20	1079.5	64.6	254	2	US-09-237-543-4
21	1079.5	64.6	254	2	US-09-644-450-4
22	869.5	52.1	311	2	US-10-184-563-2
23	869.5	52.1	372	2	US-09-949-016-7140
24	384.5	23.0	256	2	US-09-964-956-74
25	376.5	22.5	776	2	US-09-523-849-34
26	376	22.5	1101	2	US-09-770-170-8
27	370.5	22.2	778	2	US-10-116-326-2

28	370.5	22.2	778	2	US-10-003-690-2	Sequence 2, Appli
29	370.5	22.2	778	2	US-10-803-272-2	Sequence 2, Appli
30	368.5	22.1	630	2	US-10-355-975A-38	Sequence 38, Appl
31	368.5	22.1	631	2	US-09-579-664B-11	Sequence 11, Appl
32	368.5	22.1	631	2	US-10-355-975A-11	Sequence 6, Appli
33	367	22.0	1356	2	US-09-770-170-6	Sequence 72, Appl
34	364.5	21.8	256	2	US-09-964-956-72	Sequence 2, Appli
35	362.5	21.7	1323	2	US-09-770-170-2	Sequence 4, Appli
36	359	21.5	511	2	US-09-633-328B-4	Sequence 20512, A
37	358.5	21.5	281	2	US-09-248-796A-20512	Sequence 2, Appli
38	357.5	21.4	668	2	US-09-930-181-2	Sequence 2, Appli
39	357.5	21.4	668	2	US-10-054-579-2	Sequence 2, Appli
40	357.5	21.4	674	2	US-10-283-247-2	Sequence 2, Appli
41	357	21.4	512	2	US-09-633-328B-2	Sequence 7, Appli
42	353.5	21.2	674	2	US-10-283-247-7	Sequence 8, Appli
43	353.5	21.2	674	2	US-10-283-247-8	Sequence 32, Appli
44	349.5	20.9	722	2	US-08-817-832B-32	Sequence 4, Appli
45	348.5	20.9	722	2	US-09-984-890-4	

ALIGNMENTS

RESULT 1

US-09-237-543-9
; Sequence 9, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237.543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-237-543-9

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Best Local Similarity	100.0%;	Pred. No.	7.5e-161;	Mismatches	0;	Indels	0;
Matches	313;	Conservative	0;	Indels	0;	Gaps	0;
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Db	1	MLLSKINSLAHLRAAPCNDLHATKLA	PGKEKEPLESOYQVGPLLGGSGFGSVYSGIRVSD	60			
Qy	61	NLPVAIKHVEKDRISDMGELP	NGTRVPMVEVLLKKVSSGFGSGVIRLLDWFERPDSFVLIL	120			
Db	61	NLPVAIKHVEKDRISDMGELP	NGTRVPMVEVLLKKVSSGFGSGVIRLLDWFERPDSFVLIL	120			
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Db	121	BRPEVQDLFFITRGALQELARS	FWQVLEAVRHCHNCVLRHDKDENILIDNARG	180			
Qy	181	ELKIDFGSGALLKDTVTYDFD	GTFRVSPPEWIRYHRVHGRSAAVWSLIGILLYDMVCGDI	240			
Db	181	ELKIDFGSGALLKDTVTYDFD	GTFRVSPPEWIRYHRVHGRSAAVWSLIGILLYDMVCGDI	240			
Qy	241	PFEHDEEIIIRQVFFRQRVS	SECQHLIRWCLALRPSDRPTTFFEEIQNHPPMQDVLIPQETA	300			
Db	241	PFEHDEEIIIRQVFFRQRVS	SECQHLIRWCLALRPSDRPTTFFEEIQNHPPMQDVLIPQETA	300			
Qy	301	EIHLHLSLSPGSPK	313				
Db	301	EIHLHLSLSPGSPK	313				

RESULT 2

US-09-644-450-9


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; Sequence 9, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-644-450-9

Query Match 100.0%; Score 1670; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 7.5e-161; Indels 0; Gaps 0;
Matches 313; Conservative 0; Mismatches 0;

Qy 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQYQVGLLGGSGFGSVYSGIRVSD 60
Db 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQYQVGLLGGSGFGSVYSGIRVSD 60

Qy 61 NLPVAIKHVKDRISDMGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLL 120
Db 61 NLPVAIKHVKDRISDMGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLL 120

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Db 121 ERPEFVQDLFDITFERGALQELARSFFWQVLEAVRHCHNGVLRHDKDENILIDLNRG 180

Qy 181 ELKIDFGSGALLKDTVYTFDGTGRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240
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Qy 241 PFEHDEEIIIRGQVFRQVSSECOHLIRWCIALRPSDRPTPEEIQNHPPWMDVLLPOETA 300
Db 241 PFEHDEEIIIRGQVFRQVSSECOHLIRWCIALRPSDRPTPEEIQNHPPWMDVLLPOETA 300

Qy 301 EIHLSLSPGPSK 313
Db 301 EIHLSLSPGPSK 313

RESULT 3
US-08-463-081B-26
; Sequence 26, Application US/08463081B
; Patent No. 5871960
; Patent No. 5871960 5837487
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,081B
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Anzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: amino acid
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-463-081B-26

Query Match 99.2%; Score 1657; DB 1; Length 313;
Best Local Similarity 99.4%; Pred. No. 1.6e-159;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQYQVGLLGGSGFGSVYSGIRVSD 60

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Db 181 ELKIDFGSGALLKDTVYTFDGTGRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240

Qy 241 PFEHDEEIIIRGQVFRQVSSECOHLIRWCIALRPSDRPTPEEIQNHPPWMDVLLPOETA 300
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Qy 301 EIHLSLSPGPSK 313
Db 301 EIHLSLSPGPSK 313

RESULT 4
US-08-461-379A-26
; Sequence 26, Application US/08461379A
; Patent No. 5871961
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; ADDRESSEE: (B) STREET:One Westlakes-Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; APPLICATION NUMBER: US/08/461,379A
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461.379A
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; APPLICATION NUMBER: USSN 08/330,108; 08/104,736
; APPLICATION NUMBER: & 07/796,066
; FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: DART-070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)470-0700
; TELEFAX: (610)470-0701
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
; US-08-461-379A-26

Query Match 99.2%; Score 1657; DB 1; Length 313;
Best Local Similarity 99.4%; Pred. No. 1.6e-159;
Matches 311, Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 MLLSKINSLAHLRAACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

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Db 61 NLPVAIKHVEKDRISDMGELPNGTRVPMVEVLLKKVSGSPGVI RLDDWFERPDSFVLIL 120

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Db 121 ERPEVPQDLDFITFERGALQBELARSFFWQVLEAVRHCHNGCVLHRDIKDENILIDLNRG 180

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Db 181 ELKLIDFGSGALLKDTVYTFDGTGRVYSPPEWIYHRYHGHSAAVWSLGILLYDMVCGDI 240

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RESULT 5
US-08-462-390B-26
; Sequence 26, Application US/08462390B
; Patent No. 5882894
; GENERAL INFORMATION:
; APPLICANT: Smith, K. A., & Beadling, C.
; TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
; TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; ADDRESSEE: (B) STREET:One Westlakes-Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/462,390B
: FILING DATE: 5-JUNE-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USN 08/330,108
: FILING DATE: 27-OCT-1994
: APPLICATION NUMBER: USN 08/104,736
: FILING DATE: 10-AUG-1993
: APPLICATION NUMBER: USN 07/796,066
: FILING DATE: 20-NOV-91
: ATTORNEY/AGENT INFORMATION:
: NAME: Viviana Amzel, Ph. D.
: REGISTRATION NUMBER: 30,930
: REFERENCE/DOCKET NUMBER: DART-040
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (610)407-0700
: TELEFAX: (610)407-0701
: INFORMATION FOR SEQ ID NO: 26:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 313 amino acids
: TYPE: peptide
: STRANDEDNESS: n.a.
: TOPOLOGY: n.a.
: MOLECULE TYPE: peptide
: US-08-462-390B-26

Query Match          99.2%; Score 1657; DB 1; Length 313;
Best Local Similarity 99.4%; Pred. No. 1.6e-159;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0

Qy 1 MLLSKINSLAHLRAAPCNDLHATKLAGKEKEPLESQYQVCPILGSGFGSGVYSIRVSD 60
Db 1 MLLSKINSLAHLRARACNDLHATKLAGKEKEPLESQYQVCPILGSGFGSGVYSIRVSD 60
Qy 61 NLPVAIKHVEKDRISDMGELPNGTRVPMEVLLKKVSGSGFSGVIRLLDWFRRPDSFVLIL 120
Db 61 NLPVAIKHVEKDRISDMGELPNGTRVPMEVLLKKVSGSGFSGVIRLLDWFRRPDSFVLIL 120
Qy 121 ERPEPVQDLDFITERGALQEEELARSFFWQVLEAVRHCHNCGVLHARDIKDENILIDLNRG 180
Db 121 ERPEPVQDLDFITERGALQEEELARSFFWQVLEAVRHCHNCGVLHARDIKDENILIDLNRG 180
Qy 181 ELKLIIDFGSALLKQTVYTFDGTGRVYSPPEWIRYHRHYHGSSAAVWSIGILLYDMVCGDI 240
Db 181 ELKLIIDFGSALLKQTVYTFDGTGRVYSPPEWIRYHRHYHGSSAAVWSIGILLYDMVCGDI 240
Qy 241 PFEHDEEIRGQVFFRQRVSSECOHLIRWCIALRPSDRPTPEEIQNHPPMQDVLILPQETA 300
Db 241 PFEHDEEIRGQVFFRQRVSSECOHLIRWCIALRPSDRPTPEEIQNHPPMQDVLILPQETA 300
Qy 301 EIHLSLSPGFSK 313
Db 301 EIHLSLSPGFSK 313

```

RESULT 6
US-08-463-074B-26
Sequence 26, Application US/08463074B
Patent No. 6020155
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR1 Fusion Protein, Vector an
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESS: 444 South Flower St. - S
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,446
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,390
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,585
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Anzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66 40035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: peptide
STRANDEDNESS: n.a.
TOPOLOGY: n.a.
MOLECULE TYPE: peptide
US-08-652-446-26
Query Match 99.2%; Score 1657; DB 2; Length 313;
Best Local Similarity 99.4%; Pred. No. 1.6e-159;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
Db 1 MLLSKINSLAHLRAACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
Db 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
QY 121 ERPEPVQDLFDITERGALQBELARSPFWQVLEAVRHCHNCVGLHRDIKDENILIDLNRG 180
Db 121 ERPEPVQDLFDITERGALQBELARSPFWQVLEAVRHCHNCVGLHRDIKDENILIDLNRG 180
QY 181 ELKLIDFGSGALLKDTVYTPDGTTRVYSPPEWIRYHRYHGRSAAVWSLGLILYDMVCGDI 240
Db 181 ELKLIDFGSGALLKDTVYTPDGTTRVYSPPEWIRYHRYHGRSAAVWSLGLILYDMVCGDI 240
QY 241 PFEHDEEIIIRGOVFFRQVRVSSECOHLIRWCLALRPSDRPTFEEIQNHHPMQDVLVLPQETA 300
Db 241 PFEHDEEIIIRGOVFFRQVRVSSECOHLIRWCLALRPSDRPTFEEIQNHHPMQDVLVLPQETA 300
QY 301 EIHLHSLSPGPSK 313
Db 301 EIHLHSLSPGPSK 313
RESULT 9
US-09-237-543-8
; Sequence 8, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-237-543-8
Query Match 98.0%; Score 1636; DB 2; Length 313;
Best Local Similarity 97.1%; Pred. No. 2.1e-157;
Matches 304; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
Db 1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
Db 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
QY 121 ERPEPVQDLFDITERGALQBELARSPFWQVLEAVRHCHNCVGLHRDIKDENILIDLNRG 180
Db 121 ERPEPVQDLFDITERGALQBELARSPFWQVLEAVRHCHNCVGLHRDIKDENILIDLNRG 180
QY 181 ELKLIDFGSGALLKDTVYTPDGTTRVYSPPEWIRYHRYHGRSAAVWSLGLILYDMVCGDI 240
Db 181 ELKLIDFGSGALLKDTVYTPDGTTRVYSPPEWIRYHRYHGRSAAVWSLGLILYDMVCGDI 240
QY 241 PFEHDEEIIIRGOVFFRQVRVSSECOHLIRWCLALRPSDRPTFEEIQNHHPMQDVLVLPQETA 300
Db 241 PFEHDEEIIIRGOVFFRQVRVSSECOHLIRWCLALRPSDRPTFEEIQNHHPMQDVLVLPQETA 300
QY 301 EIHLHSLSPGPSK 313
Db 301 EIHLHSLSPGPSK 313
RESULT 10
US-09-644-450-8
; Sequence 8, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-644-450-8

Query Match      98.0%; Score 1636; DB 2; Length 313;
Best Local Similarity 97.1%; Pred. No. 2.1e-157;
Matches 304; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNDLHATKLAPEKEPELESQVQVGLGSGFGSGVYSGIRVSD 60
DB 1 MLLSKINSLAHLRAAPCNDLHANKLAPEKEPELESQVQVGLGSGFGSGVYSGIRVAD 60

QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
DB 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120

QY 121 ERPEPVQDLFDITFERGALQBELARSPFWQVLEAVRHCHNCGVLRHDKDENILIDLNRG 180
DB 121 ERPEPVQDLFDITFERGALQBELARSPFWQVLEAVRHCHNCGVLRHDKDENILIDLNRG 180

QY 181 ELKLIDFGSGALLKDTVYTFDGTGRVYSPPEWIRYHRYHGRSAAVWSLGIILLYDMVCGDI 240
DB 181 ELKLIDFGSGALLKDTVYTFDGTGRVYSPPEWIRYHRYHGRSAAVWSLGIILLYDMVCGDI 240

QY 241 PFEHDEEIIKQVFFRQVRVSSECOHLIRWCLALRPSDRPTPEEIQNHHPWQDVLVLPQETA 300
DB 241 PFEHDEEIVKQVFFRQVRVSSECOHLIRWCLALRPSDRPTPEEIQNHHPWQDVLVLPQETA 300

QY 301 EIHLHSLSPGSPK 313
DB 301 EIHLHSLSPGSPK 313

Query Match      94.7%; Score 1582; DB 2; Length 313;
Best Local Similarity 93.9%; Pred. No. 6.2e-152;
Matches 294; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNDLHATKLAPEKEPELESQVQVGLGSGFGSGVYSGIRVSD 60
DB 1 MLLSKINSLAHLRAAPCNDLHATKLAPEKEPELESQVQVGLGSGFGSGVYSGIRVAD 60

QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
DB 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120

QY 121 ERPEPVQDLFDITFERGALQBELARSPFWQVLEAVRHCHNCGVLRHDKDENILIDLNRG 180
DB 121 ERPEPVQDLFDITFERGALQBELARSPFWQVLEAVRHCHNCGVLRHDKDENILIDLNRG 180

QY 181 ELKLIDFGSGALLKDTVYTFDGTGRVYSPPEWIRYHRYHGRSAAVWSLGIILLYDMVCGDI 240
DB 181 ELKLIDFGSGALLKDTVYTFDGTGRVYSPPEWIRYHRYHGRSAAVWSLGIILLYDMVCGDI 240

QY 241 PFEHDEEIIKQVFFRQVRVSSECOHLIRWCLALRPSDRPTPEEIQNHHPWQDVLVLPQETA 300
DB 241 PFEHDEEIVKQVFFRQVRVSSECOHLIRWCLALRPSDRPTPEEIQNHHPWQDVLVLPQETA 300

QY 301 EIHLHSLSPGSPK 313
DB 301 EIHLHSLSPGSPK 313

RESULT 11
US-09-237-543-7
; Sequence 7, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-237-543-7

Query Match      94.7%; Score 1582; DB 2; Length 313;
Best Local Similarity 93.9%; Pred. No. 6.2e-152;
Matches 294; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNDLHATKLAPEKEPELESQVQVGLGSGFGSGVYSGIRVSD 60
DB 1 MLLSKINSLAHLRAAPCNDLHATKLAPEKEPELESQVQVGLGSGFGSGVYSGIRVAD 60

QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
DB 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120

QY 121 ERPEPVQDLFDITFERGALQBELARSPFWQVLEAVRHCHNCGVLRHDKDENILIDLNRG 180
DB 121 ERPEPVQDLFDITFERGALQBELARSPFWQVLEAVRHCHNCGVLRHDKDENILIDLNRG 180

QY 181 ELKLIDFGSGALLKDTVYTFDGTGRVYSPPEWIRYHRYHGRSAAVWSLGIILLYDMVCGDI 240
DB 181 ELKLIDFGSGALLKDTVYTFDGTGRVYSPPEWIRYHRYHGRSAAVWSLGIILLYDMVCGDI 240

QY 241 PFEHDEEIIKQVFFRQVRVSSECOHLIRWCLALRPSDRPTPEEIQNHHPWQDVLVLPQETA 300
DB 241 PFEHDEEIVKQVFFRQVRVSSECOHLIRWCLALRPSDRPTPEEIQNHHPWQDVLVLPQETA 300

QY 301 EIHLHSLSPGSPK 313
DB 301 EIHLHSLSPGSPK 313

RESULT 12
US-09-644-450-7
; Sequence 7, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-644-450-7

Query Match      94.7%; Score 1582; DB 2; Length 313;
Best Local Similarity 93.9%; Pred. No. 6.2e-152;
Matches 294; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNDLHATKLAPEKEPELESQVQVGLGSGFGSGVYSGIRVSD 60
DB 1 MLLSKINSLAHLRAAPCNDLHATKLAPEKEPELESQVQVGLGSGFGSGVYSGIRVAD 60

QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
DB 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120

QY 121 ERPEPVQDLFDITFERGALQBELARSPFWQVLEAVRHCHNCGVLRHDKDENILIDLNRG 180
DB 121 ERPEPVQDLFDITFERGALQBELARSPFWQVLEAVRHCHNCGVLRHDKDENILIDLNRG 180

QY 181 ELKLIDFGSGALLKDTVYTFDGTGRVYSPPEWIRYHRYHGRSAAVWSLGIILLYDMVCGDI 240
DB 181 ELKLIDFGSGALLKDTVYTFDGTGRVYSPPEWIRYHRYHGRSAAVWSLGIILLYDMVCGDI 240

QY 241 PFEHDEEIIKQVFFRQVRVSSECOHLIRWCLALRPSDRPTPEEIQNHHPWQDVLVLPQETA 300
DB 241 PFEHDEEIVKQVFFRQVRVSSECOHLIRWCLALRPSDRPTPEEIQNHHPWQDVLVLPQETA 300

QY 301 EIHLHSLSPGSPK 313
DB 301 EIHLHSLSPGSPK 313

RESULT 13
US-07-857-224B-41
; Sequence 41, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
```

;; COUNTRY: Switzerland
;; ZIP: (note: this is an international post code) CH-8092
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh 7.0
;; SOFTWARE: Microsoft Word
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/857,224B
;; FILING DATE: 03/25/92
;; CLASSIFICATION: 436
;; PRIOR APPLICATION DATA: none
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (International) 41 1 632 2830
;; TELEFAX: (International) 41 1 262 2437
;; TELEX: none
;; INFORMATION FOR SEQ ID NO: 41:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 257
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE:
;; DESCRIPTION: protein
;; ORIGINAL SOURCE:
;; ORGANISM: rat
;; FEATURE: Protein kinase; Table 8 Column 46
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; AUTHORS: Hanks, S. K.
;; AUTHORS: Quinn, A. M.
;; AUTHORS: Hunter, T.
;; TITLE: The protein kinase family
;; JOURNAL: Science
;; VOLUME: 241
;; PAGES: 42-52
;; DATE: 1988
;; US-07-857-224B-41

Query Match 77.6%; Score 1296.5; DB 1; Length 257;
Best Local Similarity 94.2%; Pred. No. 4.1e-123;
Matches 242; Conservative 9; Mismatches 3; Indels 3; Gaps 2;

QY 36 SOYQVGLGSGFGSVSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKK 95
DB 1 SOYQVGLGSGFGSVSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKK 58
QY 96 VSSGFGVIRLLDWPDPDSFVLIILERPVPQDLFDFTTERGALQBELARSPFWQVLEAV 155
DB 59 VSSDPSGVRLLDWPDPDSFVLIILERPVPQDLFDFTTERGALQBELARSPFWQVLEAV 118
QY 156 RHCHNCGVLRDIDKDNILIDLRGELKIDFGSGALLKDTVYTFDGTTRVYSPPEWIRY 215
DB 119 RHCHNCGVLRDIDKDNILIDLRGELKIDFGSGALLKDTVYTFDGTTRVYSPPEWIRY 178
QY 216 HRYHGRSAVWSLGLIILYDMVCGDIPF-EHDEIRGQVFFRQVRVSSECOHLIRWCLAIR 274
DB 179 HRYHGRSAVWSLGLIILYDMVCGDIPFDEHDEIRGQVFFRQVRVSSECOHLIRWCLAIR 238
QY 275 PSDRPTFEIQRNHPMQ 291
DB 239 PSDRPSFEIRNHPMQ 255

RESULT 14

US-09-237-543-2
; Sequence 2, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:

; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A

; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-237-543-2

Query Match 67.8%; Score 1133; DB 2; Length 326;
Best Local Similarity 69.3%; Pred. No. 2.1e-106;
Matches 219; Conservative 35; Mismatches 52; Indels 10; Gaps 7;

QY 1 MLLSKINSIAHLRAAP--CNDLHATKLAGK-EKEPLESOYQVGPLGSGGSGSVYSGIR 57
DB 1 MLLSKFGSLAHL-CGPGGVHDLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTYYAGSR 59
QY 58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKV--SSGFGSVIRLLDWPDPDS 115
DB 60 IADGLPVAVKHVKERVTEWGS-L-CGATVPVLEVLLRKVGAGGARGVIRLLDWPDPDG 118
QY 116 FVLILERPVPQDLFDFTTERGALQBELARSPFWQVLEAVRHCHNCGVLRDIDKDNIL 175
DB 119 FLLVLERPEPAQDLFDFTTERGALDEPLARRFFAQVLAARHCHSCGVVHRDIDKNLLV 178
QY 176 DLNRGELKIDFGSGALLKDTVYTFDGTTRVYSPPEWIRYHRYHGRSAVWSLGLIILYDM 235
DB 179 DLRSSELKIDFGSGALLKDTVYTFDGTTRVYSPPEWIRYHRYHGRSAVWSLGLVLLYDM 238
QY 236 VCGDIPFDEHDEIRGQVFFRQVRVSSECOHLIRWCLAIRPSPDPTFEIQRNHPM--QDV 293
DB 239 VCGDIPFDEHDEIRGQVFFRQVRVSSECOHLIRWCLAIRPSPDPTFEIQRNHPM--QDV 298
QY 294 LLPOETAIEIHLHSLSP 309
DB 299 GAP-ESCDRLRLCTLDP 313

RESULT 15

US-09-644-450-2
; Sequence 2, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:

; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-644-450-2

Query Match 67.8%; Score 1133; DB 2; Length 326;
Best Local Similarity 69.3%; Pred. No. 2.1e-106;
Matches 219; Conservative 35; Mismatches 52; Indels 10; Gaps 7;

QY 1 MLLSKINSIAHLRAAP--CNDLHATKLAGK-EKEPLESOYQVGPLGSGGSGSVYSGIR 57
DB 1 MLLSKFGSLAHL-CGPGGVHDLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTYYAGSR 59
QY 58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKV--SSGFGSVIRLLDWPDPDS 115
DB 60 IADGLPVAVKHVKERVTEWGS-L-CGATVPVLEVLLRKVGAGGARGVIRLLDWPDPDG 118
QY 116 FVLILERPVPQDLFDFTTERGALQBELARSPFWQVLEAVRHCHNCGVLRDIDKDNIL 175
DB 119 FLLVLERPEPAQDLFDFTTERGALDEPLARRFFAQVLAARHCHSCGVVHRDIDKNLLV 178

Qy	176	DLNRGELKIDFGGALLKDTVYTDGTRVYSPPEWIRYHRYHGRSAAVWSLGLLYDM	235
Db	179	DLRSGELKIDFGGALLKDTVYTDGTRVYSPPEWIRYHRYHGRSATVWSLGLVLLYDM	238
Qy	236	VCGDIPFEHDEIIRGQVFFRQVSSECOHLIRWCLALRPSDRPTFEEIQNHPPW--QDV	293
Db	239	VCGDIPFEODEILLRGLLFRRVSPCEQQILRWCLSLRPSERPSLDQIAAHPPWMLGADG	298
Qy	294	LLPOETAIEIHLHSLSP	309
Db	299	GAP-ESCDRLCTLDP	313

Search completed: April 21, 2006, 13:00:11
Job time : 48 secs

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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
RA Zakut-Houri R., Hazum S., Givol D., Tellerman A.;
RT "The cDNA sequence and gene analysis of the human pim oncogene.";
RN Gene 54:105-111(1987).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88217305; PubMed=3329709;
RA Domen J., von Lindern M., Hermans A., Breuer M., Grosveld G.,
RA Berns A.;
RT "Comparison of the human and mouse PIM-1 cDNAs: nucleotide sequence
RT and immunological identification of the in vitro synthesized PIM-1
RT protein.";
RN Oncogene Res. 1:103-112(1987).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88115604; PubMed=3429489;
RA Meeker T.C., Nagarajan L., Ar-Rushdi A., Croce C.M.;
RT "Cloning and characterization of the human PIM-1 gene: a putative
RT oncogene related to the protein kinases.";
RN J. Cell. Biochem. 35:105-112(1987).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Asavant T.L., Scheetz T.E.
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lomuellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.

RN NUCLEOTIDE SEQUENCE.
RA Laid G.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AL353579; CAI20316.1; -; Genomic DNA.
DR SMR; Q57H7; 32-308.
DE* Ensembl; ENSG00000137193; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 313 AA; 35686 MW; 35BA76D3668E69A3 CRC64;

Query Match 100.0%; Score 1670; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 7.2e-115;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEPLESQYQVGLLGGSGFGSVYSGIRVSD 60
DB 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEPLESQYQVGLLGGSGFGSVYSGIRVSD 60
QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
DB 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
QY 121 ERPEVQDLDFITRGALQBELARSFQVLEAVRHCHNCVGLHRDKDENILIDLNRG 180
DB 121 ERPEVQDLDFITRGALQBELARSFQVLEAVRHCHNCVGLHRDKDENILIDLNRG 180
QY 181 ELKLIDFGSGALLKDTVTYDFDGTGRVYSPPEWIRYHRYHGSAAVWSLGLLYDMVCGDI 240
DB 181 ELKLIDFGSGALLKDTVTYDFDGTGRVYSPPEWIRYHRYHGSAAVWSLGLLYDMVCGDI 240
QY 241 PFEHDEEIIIRGQVFRQRVSSECOHLIRWCLALRPSDRPTFEEIQNHHPMDVLLPQETA 300
DB 241 PFEHDEEIIIRGQVFRQRVSSECOHLIRWCLALRPSDRPTFEEIQNHHPMDVLLPQETA 300
QY 301 EIHLSLSPGFSK 313
DB 301 EIHLSLSPGFSK 313

RESULT 3
PIM1_FELCA STANDARD; PRT; 313 AA.
AC Q95LJ0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN Name=PIM1;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fujino Y., Satoh H., Hisasue M., Masuda K., Ohno K., Tsujimoto H.;

RT "The cDNA sequence of the feline pim-1 oncogene.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -|- SUBUNIT: Binds to RP9 (By similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -|- PTM: Autophosphorylated (By similarity).
CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM subfamily.

CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

DR EMBL; AB073748; BAB71752.1; -; mRNA.
DR SMR; Q95LJ0; 32-308.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase; Transferase.
KW DOMAIN 38 290 Protein kinase.
FT NP_BIND 44 52 ATP (By similarity).
FT ACT_SITE 167 167 Proton acceptor (By similarity).
FT BINDING 67 67 ATP (By similarity).
SQ SEQUENCE 313 AA; 35686 MW; C0BE268D638E6967 CRC64;

Query Match 99.3%; Score 1659; DB 1; Length 313;
Best Local Similarity 99.0%; Pred. No. 4.6e-114;
Matches 310; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEPLESQYQVGLLGGSGFGSVYSGIRVSD 60
DB 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEPLESQYQVGLLGGSGFGSVYSGIRVSD 60
QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
DB 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
QY 121 ERPEVQDLDFITRGALQBELARSFQVLEAVRHCHNCVGLHRDKDENILIDLNRG 180
DB 121 ERPEVQDLDFITRGALQBELARSFQVLEAVRHCHNCVGLHRDKDENILIDLNRG 180
QY 181 ELKLIDFGSGALLKDTVTYDFDGTGRVYSPPEWIRYHRYHGSAAVWSLGLLYDMVCGDI 240
DB 181 ELKLIDFGSGALLKDTVTYDFDGTGRVYSPPEWIRYHRYHGSAAVWSLGLLYDMVCGDI 240
QY 241 PFEHDEEIIIRGQVFRQRVSSECOHLIRWCLALRPSDRPTFEEIQNHHPMDVLLPQETA 300
DB 241 PFEHDEEIIIRGQVFRQRVSSECOHLIRWCLALRPSDRPTFEEIQNHHPMDVLLPQETA 300
QY 301 EIHLSLSPGFSK 313
DB 301 EIHLSLSPGFSK 313

RESULT 4
PIM1_BOVIN STANDARD; PRT; 313 AA.
AC Q9N0P9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN Name=PIM1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21109090; PubMed=1182156; DOI=10.1016/S0165-2427(00)00259-2;
RA Wang Z., Petersen K., Weaver M.S., Magnuson N.S.;
RT "cDNA cloning, sequencing and characterization of bovine pim-1.";
RL Vet. Immunol. Immunopathol. 78:177-195(2001).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Binds to RP9 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -!- PTM: Autophosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF259078; AAF67200.1; -; mRNA.
CC HSSP; O63450; 1A06.
CC SMR; O5N0P9; 32-308.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR008271; Ser Thr_pkin_AS.
CC Pfam; PF00069; Pkinase; 1.
CC ProDom; PD000001; Prot kinase; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW Transferrase.
FT DOMAIN 38 290 Protein kinase.
FT NP_BIND 44 52 ATP (By similarity).
FT ACT_SITE 167 167 Proton acceptor (By similarity).
FT BINDING 67 67 ATP (By similarity).
SQ SEQUENCE 313 AA; 35630 MW; 9EF40229A847AD47 CRC64;

Query Match 99.2%; Score 1656; DB 1; Length 313;
Best Local Similarity 98.7%; Pred. No. 7.7e-114;
Matches 309; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNLDHATKLAPGKEKEPLESOYQVGLGSGFGSVYSGIRVSD 60
Db 1 MLLSKINSLAHLRAAPCSDLHATKLAPGKEKEPLESOYQVGLGSGFGSVYSGIRVAD 60

QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVLLKKVSSGFGSVIRLLDWFPERPDSFVLIL 120
Db 61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVLLKKVSSGFGSVIRLLDWFPERPDSFVLIL 120

QY 121 ERPEPVQDLFDFTTERGALQELARSPFWQVLEAVRHCHNCGVLRHDKDENILIDLNRG 180
Db 121 ERPEPVQDLFDFTTERGALQELARSPFWQVLEAVRHCHNCGVLRHDKDENILIDLNRG 180

QY 181 ELKLIDFGSGALLKDTVTYDFDGTIRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240
Db 181 ELKLIDFGSGALLKDTVTYDFDGTIRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240

QY 301 EHLHSLSPGSK 313
Db 301 EHLHSLSPGSK 313

RESULT 5
PIM1_RAT STANDARD; PRT; 313 AA.
ID PIM1_RAT
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AC P26794;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN Name=Pim1; Synonyms=Pim-1;
OS Rattus norvegicus (Rat).
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=92319652; PubMed=1620615;
RA Wingett D., Reeves R., Magnuson N.S.;
RT "Characterization of the testes-specific pim-1 transcript in rat.";
RL Nucleic Acids Res. 20:3183-3189(1992).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Binds to RP9 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -!- PTM: Autophosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X63675; CAA45214.1; -; mRNA.
CC PIR; S26298; S26298.
CC SMR; F26794; 32-308.
CC Ensembl; ENSRNOG00000000529; Rattus norvegicus.
CC RGD; 3330; Pim1.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR008271; Ser Thr_pkin_AS.
CC Pfam; PF00069; Pkinase; 1.
CC ProDom; PD000001; Prot kinase; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW Transferrase.
FT DOMAIN 38 290 Protein kinase.
FT NP_BIND 44 52 ATP (By similarity).
FT ACT_SITE 167 167 Proton acceptor (By similarity).
FT BINDING 67 67 ATP (By similarity).
SQ SEQUENCE 313 AA; 35631 MW; D5757DA9F1821BF9 CRC64;

Query Match 98.0%; Score 1636; DB 1; Length 313;
Best Local Similarity 97.1%; Pred. No. 2.3e-112;
Matches 304; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNLDHATKLAPGKEKEPLESOYQVGLGSGFGSVYSGIRVSD 60
Db 1 MLLSKINSLAHLRAAPCNLDHATKLAPGKEKEPLESOYQVGLGSGFGSVYSGIRVAD 60

QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVLLKKVSSGFGSVIRLLDWFPERPDSFVLIL 120
Db 61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVLLKKVSSGFGSVIRLLDWFPERPDSFVLIL 120

QY 121 ERPEPVQDLFDFTTERGALQELARSPFWQVLEAVRHCHNCGVLRHDKDENILIDLNRG 180
Db 121 ERPEPVQDLFDFTTERGALQELARSPFWQVLEAVRHCHNCGVLRHDKDENILIDLNRG 180

QY 181 ELKLIDFGSGALLKDTVTYDFDGTIRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240
Db 181 ELKLIDFGSGALLKDTVTYDFDGTIRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240

QY 241 PFEHDEEIRGVFRQVRVSSCOHLIRWCLALRPSDRPTFEEIQNHPPMQDVLVLPQETA 300
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Db 241 PFEHDEIVKGVYRQRVSSECHLRWCLSLRSDRSPSEIQQNHFWMDVLLPQATA 300
Qy ~ 301 EIHLSLSPGSPK 313
Db 301 EIHLSLSPGSPK 313

RESULT 6
QBCFN8_MOUSE
ID QBCFN8_MOUSE PRELIMINARY; PRT; 313 AA.
AC QBCFN8;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Proviral integration site 1.
GN Name=Pim1;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain, and Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RA Strausberg R.;
RN Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RN Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
[4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RN Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC042885; AAH42885.1; -; mRNA.
DR EMBL; BC053019; AAH53019.1; -; mRNA.
DR EMBL; BC055316; AAH55316.1; -; mRNA.
DR SMC; QBCFN8; 32-308.
DR Ensembl; ENSMUSG00000024014; Mus musculus.
DR MG1; MG1:97584; Pim1.
DR GO; GO:000524; P:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
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DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SMO0220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 313 AA; 35451 MW; 1294F16A03B7C7D7 CRC64;

Query Match 95.0%; Score 1587; DB 2; Length 313;
Best Local Similarity 94.2%; Pred. No. 9.3e-109;
Matches 295; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MLLSKINSLAHLRAAPCNLDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSGYSGIRVSD 60
Db 1 MLLSKINSLAHLRAAPCNLDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSGYSGIRVAD 60
Qy 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
Db 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
Qy 121 ERPSVQDLDFITERRGALQELARSPFQVLEAVRHCHNCVGLHRDKDENILIDLNRG 180
Db 121 ERPSVQDLDFITERRGALQELARSPFQVLEAVRHCHNCVGLHRDKDENILIDLNRG 180
Qy 181 ELKLIDFGSGALLKDTVYTFDGTFRVYSPPEWIRYHGRSAAVWSLGLILLYDMVCGDI 240
Db 181 ELKLIDFGSGALLKDTVYTFDGTFRVYSPPEWIRYHGRSAAVWSLGLILLYDMVCGDI 240
Qy 241 PFEHDEIIRQVFRVRSSECHLRWCLSLRSDRSPSEIQQNHFWMDVLLPQETA 300
Db 241 PFEHDEIIRQVFRVRSSECHLRWCLSLRSDRSPSEIQQNHFWMDVLLPQETA 300
Qy 301 EIHLSLSPGSPK 313
Db 301 EIHLSLSPGSPK 313

RESULT 7
PIM1_MOUSE
ID PIM1_MOUSE STANDARD; PRT; 313 AA.
AC P06803;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN Name=Pim1; Synonyms=Pim-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
RA Selden G., Cuypers H.T., Boelens W., Robanus-Maandag E., Verbeek J.,
Donen J., van Beveren C., Berns A.;
RT "The primary structure of the putative oncogene pim-1 shows extensive
homology with protein kinases."
RL Cell 46:603-611 (1986).
RN [2]
RP INTERACTION WITH RP9.
RX MEDLINE=20389540; PubMed=10931201;
RA Maita H., Harada Y., Negakubo D., Kitauro H., Ikeda M., Tamai K.,
Takahashi K., Ariga H., Iguchi-Arigo S.M.M.;
RT "PAP-1, a novel target protein of phosphorylation by Pim-1 kinase."
RL Eur. J. Biochem. 267:5168-5178 (2000).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Binds to RP9.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
```


AC Q86V86; O68B2;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT -13-SEP-2005 (Rel. 48, Last annotation update)
 DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
 GN Names=PIM3;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY.
 RC TISSUE=liver;
 RX PubMed=15540201; DOI=10.1002/ijc.20719;
 RA Fujii C., Nakamoto Y., Lu P., Tsuneyama K., Popivanova B.K.,
 RA Kaneko S., Mukaida N.;
 RT "Aberrant expression of serine/threonine kinase Pim-3 in
 RT hepatocellular carcinoma development and its role in the proliferation
 RT of human hepatoma cell lines.";
 RL Int. J. Cancer 114:209-218(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP IDENTIFICATION FROM ESTS.
 RX MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6;
 RA Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.;
 RT "Consistency checks for characterizing protein forms.";
 RL Comput. Biol. Chem. 27:29-35(2003).
 CC -!- FUNCTION: May be involved in cell cycle progression and anti-
 CC apoptosis process. Implicated in proliferation of human hepatoma
 CC cell lines.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- TISSUE SPECIFICITY: Widely expressed. No expression in colon,
 CC thymus, and small intestine. Expressed in human hepatoma cell
 CC lines but not in normal liver tissues.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
 CC subfamily.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AB114795; BAD2438.1; -; mRNA.
 CC ENSEMBL; BC052239; -; NOT ANNOTATED CDS; mRNA.
 CC ENSEMBL; ENSG00000198355; Homo sapiens.
 CC HGNC; HGNC:19310; PIM3.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR008271; Ser_thr_kin_AS.

DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Nucleotide-Binding; Phosphorylation;
 KW Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 40 293 Protein kinase.
 FT NP_BIND 46 54 ATP (By similarity).
 FT ACT_SITE 170 170 Proton acceptor (By similarity).
 FT BINDING 69 69 ATP (By similarity).
 SQ SEQUENCE 326 AA; 35863 MW; 41FDF9DD2467A162 CRC64;
 Query Match 67.8%; Score 1133; DB 1; Length 326;
 Best Local Similarity 69.3%; Pred. No. 2.6e-75;
 Matches 219; Conservative 35; Mismatches 52; Indels 10; Gaps 7;
 QY 1 MLLSKINSLAHLRAAP--CNDLHATKLPQK-EKEPLESOYQVGLPGSGGPGSVSGIR 57
 DB 1 MLLSKFGSLAHL-CGPGVDHLPVKILOPAKADKESFEKAYQGVGLGSGGFGTVVAGSR 59
 QY 58 VSDNLPVAIKHVEKDRISDWGELPNCGRVPMVEYLLKKV--SSGFGSVIRLLDWERPDS 115
 DB 60 IADGLPVAVKVVKERVTEWGS-L-GGATVPLEVLLRKVGAAGGARGVIRLLDWERPDS 118
 QY 116 FVILLRPEPVQDLDFITFERGALQEELARSFQWQVLEAVRHCHNCVGLHRIKDNILI 175
 DB 119 FLVLVLRPEPAQDLDFITFERGALDEPLARRFFPAQVLAARVHCHSCGVVHRDKENLLV 178
 QY 176 DLNRGELKLIIDFGSGALLKDTVTDFGTRVSPPEWIRVYHGRSAAVWSIGILLYDM 235
 DB 179 DLRSGLKLIIDFGSGALLKDTVTDFGTRVSPPEWIRVYHGRSAATVWSIGVLLYDM 238
 QY 236 VCGDIPFEHDEEIIIRQVFFRQVRSSECOHLRWCLALRPSDRPTPEEQNHQPMW--QDV 293
 DB 239 VCGDIPFEQDEEILRGRLFRRRVSPCCQLRWCLSRPSRPSRPSLDQIAAHPMLGADG 298
 QY 294 LLPQETAETHLSLP 309
 DB 299 GAP-EESCDRLRLCTLD 313
 RESULT 10
 PIM3_MOUSE STANDARD; PRT; 326 AA.
 AC P58750;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
 GN Names=Pim3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=FVB/N; TISSUE=Colon, and Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,


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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
RA Butterfield V.S.N., Kzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BC017621; AAH17621.1; -; mRNA.
DR EMBL; BC026639; AAH26639.1; -; mRNA.
DR HSSP; Q03656; 1HOW.
DR Ensembl; ENSMUSG00000035828; Mus musculus.
DR MGI; MGI:1355237; Pim3.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 40 293 Protein kinase.
FT NP_BIND 46 54 ATP (By similarity).
FT ACT_SITE 170 170 Proton acceptor (By similarity).
FT BINDING 69 69 ATP (By similarity).
SQ SEQUENCE 326 AA; 35970 MW; DD68CBF46354851E CRC64;

Query Match 67.6%; Score 1129.5; DB 1; Length 326;
Best Local Similarity 72.2%; Pred. No. 4.8e-75;
Matches 213; Conservative 31; Mismatches 44; Indels 7; Gaps 5;

QY 1 MLISKINSLAHLRAAP--CNDLHATKLPAGK-EKEPLESOYQVGPLSGGFGSVYSGIR 57
Db 1 MLUSKFGSLAHL-CGPGGVHDLPVKILOPAKADKSEFEKYQVGAVLGGSGFGTVAGSR 59

QY 58 VSDNLPVAIKHVKDRISDWGELPNGTRVPMVEVLLKKV--SSGFGSVIRLLDWFPERPDS 115
Db 60 IADGLPVAVKHVVKERVTEWGSLL-GGVAVPVLVLLRKVGAAGARGVIRLLDWFPERPDG 118

QY 116 FVILRPEPVDLPDFFITERGALQBELARSFQWVLEAVRHCHNGCVLHRDKDENILI 175
Db 119 FLVLRLRPEPAQDLDFDFFITERGALDEPLARRFPAQVLAARVHCHNGGVVHRDIDKENLIV 178

QY 176 DLNRGELKIDFGSGALLQDVTYDFGRVYSPPEWIRVYHGRSAVWSIGLLYDM 235
Db 179 DLRSGLKIDFGSGAVLKQDVTYDFGRVYSPPEWIRVYHGRSATVWSIGLVLYDM 238

QY 236 VCGDIPFEHDEETIRQVFRFRVSQCQHLIRWCLALRPSRPTPEETIQNHPPM 290
Db 239 VCGDIPFEQDEETIRGLFRFRVRSPECQQLIEWCLSLRPSRPSLDQIAAHPWM 293

RESULT 11
PIM3-RAT
ID PIM3 RAT STANDARD; PRT; 326 AA.
AC Q70424;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Protein kinase
DE Kid-1) (Kinase induced by depolarization).
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QY 176 DLNRGELKLIIDFGSGALLKDTVTYDFDGTGRVSPPEWIRYHRYHGRSAAVWSIGLLYDM 235
DB 179 DLRSGLKLIIDFGSGAVLKDTVTYDFDGTGRVSPPEWIRYHRYHGRSAAVWSIGLLYDM 238
QY 236 VCGDIPFEHDEEIIHQVFFRQVRSSCQHLIRWCLALRPSDPTTPEEIQNHPPM 290
DB 239 VCGDIPFEQDEEILRGRLFFRRVSPCCQQLIEWCLSLRPSRPSLDQIAAHPWM 293

RESULT 12
Q4V8M2 RAT PRELIMINARY; PRT; 380 AA.
AC Q4V8M2;
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DE Hypothetical protein (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klanner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smaluk D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RG NIH MGC Project;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: BC097317; AAH97317.1; -; mRNA.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR008271; Ser_Thr_pkin_AS.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00101; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferrase.
FT NON_TER
SQ SEQUENCE 380 AA; 41568 MW; F82B8E50DD71346 CRC64;

Query Match 67.6%; Score 1128.5; DB 2; Length 380;
Best Local Similarity 72.2%; Pred. No. 6.8e-75;
Matches 213; Conservative 31; Mismatches 44; Indels 7; Gaps 5;

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QY 1 MLLSKINSLAHLRAAP--CNDLHATKLAPEG-EKEPLESOYQVGLGSGFGSVYSGR 57
DB 55 MLLSKFSGSLAHL-CGPGVDHLPVKILOPAKADKESFEKYQVGAVLGSGFGFTVAGSR 113
QY 58 VSDNLPVAIKHVEKORISDWGELPNGTRVPMVLLKKV--SSGFGVIRLLDWFERPDS 115
DB 114 IADGLFVAVKVVKERVTEWGS-L-CGMAVPELVLLRKVKGAAGCAGVIRLLDWFERPDS 172
QY 116 FVLILRPERPVDLFDITFERGALQELARSFPWQVLEAVRHCHNCGVLRDIDKENILI 175
DB 173 FLVLRLRPERPAQDLFDITFERGALDEPLARFFAQVLAARHCHNCGVLRDIDKENILI 232
QY 176 DLNRGELKLIIDFGSGALLKDTVTYDFDGTGRVSPPEWIRYHRYHGRSAAVWSIGLLYDM 235
DB 233 DLRSGLKLIIDFGSGAVLKDTVTYDFDGTGRVSPPEWIRYHRYHGRSAAVWSIGLLYDM 292
QY 236 VCGDIPFEHDEEIIHQVFFRQVRSSCQHLIRWCLALRPSDPTTPEEIQNHPPM 290
DB 293 VCGDIPFEQDEEILRGRLFFRRVSPCCQQLIEWCLSLRPSRPSLDQIAAHPWM 347

RESULT 13
Q811X8 MOUSE PRELIMINARY; PRT; 325 AA.
AC Q811X8;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE KID1.
GN Names=Pim3; Synonyms=Kidl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yu L.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AY026239; AAK16606.1; -; mRNA.
DR HSSP: Q03656; 1Q99.
DR SWR: O811X8; 36-292.
DR MGI: MGI:1355297; Pim3.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR008271; Ser_Thr_pkin_AS.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot kinase; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferrase.
SQ SEQUENCE 325 AA; 35931 MW; 77DEF8E20F41E3F4 CRC64;

Query Match 66.8%; Score 1116; DB 2; Length 325;
Best Local Similarity 71.9%; Pred. No. 4.7e-74;
Matches 212; Conservative 32; Mismatches 43; Indels 8; Gaps 6;

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QY 1 MLLSKINSLAHLRAAP--CNDLHATKLAPEG-EKEPLESOYQVGLGSGFGSVYSGR 57
DB 1 MLLSKFSGSLAHL-CGPGVDHLPVKILOPAKADKESFEKYQVGAVLGSGFGFTVAGSR 59
QY 58 VSDNLPVAIKHVEKORISDWGELPNGTRVPMVLLKKV--SSGFGVIRLLDWFERPDS 115
DB 60 IADGLFVAVKVVKERVTEWGS-L-CGMAVPELVLLRKVKGAAGCAGVIRLLDWFERPDS 118
QY 116 FVLILRPERPVDLFDITFERGALQELARSFPWQVLEAVRHCHNCGVLRDIDKENILI 175
DB 119 FLVLRLRPERPAQDLFDITFERGALDEPLARFFAQVLAARHCHNCGVLRDIDKENILI 178

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QY 176 DLNRGELKIDFGSGALLKOTVYTDGTRVSPPEWIRYHRYHGRSAAVWSLGLLYDM 235
DB 179 DLRSGLKIDFGSGAVLKOTVYTDGTRVSPPEWIRYHRYHGRSAATVWSLGLLYDM 238

QY 236 VCGDIPFDEHDEEIRQVFFRQVRVSECOHLRWCLALRPSDRPTPEEIQNHPPWM 290
DB 239 VCGDIPFDEHDEEIRGLFRRRVSPCCQQLIEWCLSLRPSRPSLDKL-CHPPWM 292

RESULT 14
PIM3_XENLA
ID PIM3_XENLA STANDARD; PRT; 323 AA.
AC Q91822;
DT 15-DEC-1998 (rel. 37, Created)
DT 15-DEC-1998 (rel. 37, Last sequence update)
DT 13-SEP-2005 (rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Pim-1).
GN Name=PIM3; Synonyms=PIM1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RC NUCLEOTIDE SEQUENCE, AND PHOSPHORYLATION SITES.
RP MEDLINE=97256766; PubMed=9099695; DOI=10.1074/jbc.272.16.10514;
RA Palaty C.K., Kalmr G., Tai G., Oh S., Amankawa L., Affolter M.,
RA Aebersold R., Pelech S.L.;
RT Identification of the autophosphorylation sites of the Xenopus laevis
Pim-1 proto-oncogene-encoded protein kinase.";
RL J. Biol. Chem. 272:10514-10521(1997).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- PTM: Autophosphorylated.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
subfamily.
CC -!- CAUTION: Was originally (Ref.1) called Pim-1 but seems to
represent the pim-3 isoform.
-----
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removed.
-----
DR EMBL; L29495; AA85389.1; -; mRNA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser thr pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 40 291
FT NP_BIND 46 54
FT ACT_SITE 168 168
FT BINDING 69 69
FT MOD_RES 4 4
FT *
FT MOD_RES 190 190
FT MOD_RES 205 205
FT *
SQ SEQUENCE 323 AA; 36964 MW; AB4DD61E7A99A38F CRC64;
Query Match 66.2%; Score 1105; DB 1; Length 323;
Best Local Similarity 65.3%; Pred. No. 3e-73;
Matches 205; Conservative 47; Mismatches 50; Indels 12; Gaps 5;

QY 1 MLLSKINSLAHRAAPCN-----DLHATKLAFGK-EKEPLESOYQVGLGSGFGSVYS 54
DB 1 MLLSKFGSLAHI-----CNPSNMHLPVKILQPKVDKEPFEKVYQVGSVWASGSGFGTVYS 56

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QY 55 GURVSDNLPAIKHVEKDRISDWGELPNCITRVPMVEVLLKKVSSGFGVIRLLDWPERD 114
DB 57 DSIADQCPVAVKHAKERVTEWGL-NGVWPVLEIVLLKKVTAERGVINLTDWTERPD 115

QY 115 SFVLILREPEPVQDLFDFTITERGALQEELARSPFMQVLEAVRHCHNCVGLHRDKDENIL 174
DB 116 AFLIVMERPEPVKDLFDYITEKGPLDEDTARGFFRQVLEAVRHCHNCVGVVHRDKDENL 175

QY 175 IDLNRGELKIDFGSGALLKOTVYTDGTRVSPPEWIRYHRYHGRSAAVWSLGLLYD 234
DB 176 VDRNGELKIDFGSGALLKOTVYTDGTRVSPPEWIRYHRYHGRSAATVWSLGLLYD 235

QY 235 MYCGDIPFDEHDEEIRQVFFRQVRVSECOHLRWCLALRPSDRPTPEEIQNHPPWM-ODV 293
DB 236 MYGDIPEQDEEIVRVLRCFRRISTECCQLIKWCLSLRPSDRPTLEQIFDHPWMCCKD 295

QY 294 LLPQETAETIHLHL 307
DB 296 LVKSEDCDLRLRTI 309

RESULT 15
Q66I11_XENTR
ID Q66I11_XENTR PRELIMINARY; PRT; 318 AA.
AC Q66I11;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Pim3-prov protein.
GN Name=pim3-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC081340; AAH81340.1; -; mRNA.
DR SMR; Q66I11; 32-297
DR Ensemble; ENSXGTG0000009354; Xenopus tropicalis.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.

```

Search completed: April 21, 2006, 12:58:33
Job time : 230 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 21, 2006, 12:54:54 ; Search time 40 Seconds
(without alignments)
752.896 Million cell updates/sec

Title: US-10-664-421-1

Perfect score: 1670

Sequence: 1 MLLSKINSLAHLRAAPCNDL.....LLPQETAETHLSLSPGSPK 313

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1670	100.0	313	1 TVHUP1	protein kinase (EC
2	1636	98.0	313	1 S26298	protein kinase (EC
3	1582	94.7	313	1 TVNSP1	protein kinase (EC
4	881.5	52.8	370	1 S55333	protein kinase pim
5	617	36.9	363	2 T22255	hypothetical prote
6	486	29.1	409	2 T15435	hypothetical prote
7	386	23.1	481	2 I49072	protein kinase - m
8	330	22.8	1398	2 T13741	hypothetical prote
9	376	22.5	1101	2 S66730	hypothetical prote
10	367	22.0	1358	2 S33653	probable serine/th
11	366	21.9	504	2 T10449	probable serine/th
12	361	21.6	651	2 S52244	p69Eg3 protein - A
13	361	21.6	798	2 JC7500	qik protein - chic
14	360	21.6	512	1 JC1446	serine/threonine-s
15	359	21.5	511	1 A56009	serine/threonine-s
16	357	21.4	512	2 T52633	serine/threonine-s
17	352	21.1	512	2 T07788	probable serine/th
18	348	20.8	472	2 B90100	SNF-related kinase
19	347.5	20.8	469	2 B84644	probable protein k
20	347.5	20.8	887	2 T20941	hypothetical prote
21	345	20.7	726	2 T33998	hypothetical prote
22	342.5	20.5	489	2 T04862	probable serine/th
23	342.5	20.5	1558	2 T23253	hypothetical prote
24	341.5	20.4	414	2 JN0323	Ca2+/calmodulin-de
25	341	20.4	513	1 S60304	serine/threonine-s
26	339.5	20.3	504	2 T07415	probable serine/th
27	337	20.2	502	2 T02306	probable protein k
28	337	20.2	713	2 T27966	probable serine/th
29	336.5	20.1	445	2 S20802	serine/threonine p

30	335	20.1	745	2 G01025	serine/threonine p
31	333.5	20.0	1518	2 S37928	probable purine nu
32	331.5	19.9	774	2 I48609	probable serine/th
33	331	19.8	435	2 E84707	probable protein k
34	330.5	19.8	339	2 S56719	serine/threonine-s
35	330.5	19.8	520	2 G86414	probable protein k
36	330.5	19.8	553	1 T02139	calcium-dependent
37	328	19.6	591	2 S54788	calcium-stimulated
38	327	19.6	582	2 E84721	probable calcium-d
39	326.5	19.6	746	2 S62365	SNF1-related prote
40	325.5	19.5	442	2 T48203	hypothetical prote
41	325	19.5	1246	2 G89287	protein H39e23.1 [
42	324.5	19.4	713	2 T37886	probable serine/th
43	324	19.4	401	2 B90120	SNF1-related prote
44	323	19.3	461	2 T14822	probable serine/th
45	323	19.3	473	1 S59941	serine/threonine-s

ALIGNMENTS

RESULT 1

TVHUP1

N: protein kinase (EC 2.7.1.37) pim-1 - human

C: Species: Homo sapiens (man)

C: Date: 31-Mar-1989 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C: Accession: JU0327; A46554; A27476; I58412

R: Reeves, R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.

Gene 90, 303-307, 1990

A: Title: Primary structure of the putative human oncogene, pim-1.

A: Reference number: JU0327; MUID:90382681; PMID:2205533

A: Accession: JU0327

A: Molecule type: DNA

A: Residues: 1-313 <RES>

A: Cross-references: UNIPROT:P11309; UNIPARC:UPI000001060; GB:M27903; NID:g189958; PIDN

R: Meeker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M.

J. Cell. Biochem. 35, 105-112, 1987

A: Title: Cloning and characterization of the human PIM-1 gene: a putative oncogene rela

A: Reference number: A46554; MUID:88115604; PMID:3429489

A: Accession: A46554

A: Molecule type: mRNA

A: Residues: 1-313 <RES>

A: Cross-references: UNIPARC:UPI000001060; GB:M24779; NID:g1066790; PIDN:AAA81553.1; PID

R: Zakut-Houri, R.; Hazum, S.; Gliwol, D.; Teferman, A.

Gene 54, 105-111, 1987

A: Title: The cDNA sequence and gene analysis of the human pim oncogene.

A: Reference number: A27476; MUID:87277423; PMID:3475233

A: Accession: A27476

A: Molecule type: mRNA

A: Residues: 1-14, 'RA', 17-313 <ZAK>

A: Cross-references: UNIPARC:UPI00014987C; GB:M16750; NID:g189956; PIDN:AAA60089.1; PID

R: Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.

Oncogene Res. 1, 103-112, 1987

A: Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immunol

A: Reference number: I58412; MUID:88217305; PMID:3329709

A: Accession: I58412

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: mRNA

A: Residues: 1-313 <DOM>

A: Cross-references: UNIPARC:UPI000001060; GB:M54915; NID:g189961; PIDN:AAA36447.1; PID

C: Comment: Pim-1 autophosphorylates at unknown sites.

C: Genetics:

A: Gene: GDB:PIM1

A: Cross-references: GDB:119495; OMIM:164960

A: Map position: 6p21.2-6p21.2

A: Introns: 28/2; 63/3; 80/3; 203/1; 262/1

C: Function:

A: Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni

C: Superfamily: kinase-related transforming protein; protein kinase homology

C: Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen

F: 36-290/Domain: protein kinase homology <KIN>

F: 44-52/Region: protein kinase ATP-binding motif

F:67/Active site: Lys #status predicted

Query Match 100.0%; Score 1670; DB 1; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.9e-76;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNLDLHATKAPGKEPLESOYQVGPLLGGGFGSVYSGIRVSD 60
DB 1 MLLSKINSLAHLRAAPCNLDLHATKAPGKEPLESOYQVGPLLGGGFGSVYSGIRVSD 60
QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
DB 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
QY 121 ERPEPVQDLFDPIITRGALQOEELARSFQVQVLEAVRHCHNCVGLHRDIKDENILIDLNRG 180
DB 121 ERPEPVQDLFDPIITRGALQOEELARSFQVQVLEAVRHCHNCVGLHRDIKDENILIDLNRG 180
QY 181 ELKLDIFGSGALLKDTVTYDFDGTTRYVSPPEWIRVHRHGSAAVWSLGLLYDMVCGDI 240
DB 181 ELKLDIFGSGALLKDTVTYDFDGTTRYVSPPEWIRVHRHGSAAVWSLGLLYDMVCGDI 240
QY 241 PREHDEEIRGQVFRQVRVSSCOHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPLQETA 300
DB 241 PREHDEEIRGQVFRQVRVSSCOHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPLQETA 300
QY 301 EHLHSLSPGSPK 313
DB 301 EHLHSLSPGSPK 313

RESULT 2

S26298
protein kinase (EC 2.7.1.37) pim-1 - rat
N:Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote
C:Species: Rattus norvegicus (Norway rat)
C>Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C:Accession: S26298
R:Wingett, D.; Reeves, R.; Magnuson, N.S.
Nucleic Acids Res. 20, 3183-3189, 1992
A:Title: Characterization of the testes-specific pim-1 transcript in rat.
A:Reference number: S26298; MUID:92319652; PMID:1620615
A:Accession: S26298
A:Molecule type: mRNA
A:Residues: 1-313 <WIN>
A:Experimental source: testis
A:Note: testis-specific transcript is shorter and more stable than the somatic transcrip
C:Comment: Pim-1 autophosphorylates at unknown sites.
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Note: in testis may be involved in signal transduction events of normal germ cell matu
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F:36-290/Domain: protein kinase homology <KIN>
F:44-52/Region: protein kinase ATP-binding motif
F:67/Active site: Lys #status predicted

Query Match 98.0%; Score 1636; DB 1; Length 313;
Best Local Similarity 97.1%; Pred. No. 9.2e-75;
Matches 304; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNLDLHATKAPGKEPLESOYQVGPLLGGGFGSVYSGIRVSD 60
DB 1 MLLSKINSLAHLRAAPCNLDLHATKAPGKEPLESOYQVGPLLGGGFGSVYSGIRVAD 60
QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
DB 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
QY 121 ERPEPVQDLFDPIITRGALQOEELARSFQVQVLEAVRHCHNCVGLHRDIKDENILIDLNRG 180
DB 121 ERPEPVQDLFDPIITRGALQOEELARSFQVQVLEAVRHCHNCVGLHRDIKDENILIDLNRG 180

QY 181 ELKLDIFGSGALLKDTVTYDFDGTTRYVSPPEWIRVHRHGSAAVWSLGLLYDMVCGDI 240
DB 181 ELKLDIFGSGALLKDTVTYDFDGTTRYVSPPEWIRVHRHGSAAVWSLGLLYDMVCGDI 240
QY 241 PREHDEEIRGQVFRQVRVSSCOHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPLQETA 300
DB 241 PREHDEEIRGQVFRQVRVSSCOHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPLQETA 300
QY 301 EHLHSLSPGSPK 313
DB 301 EHLHSLSPGSPK 313
RESULT 3
TWSPI
protein kinase (EC 2.7.1.37) pim-1 - mouse
N:Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote
C:Species: Mus musculus (house mouse)
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C:Accession: A24169
R:Seiten, G.; Cuyper, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; v
Cell 46, 603-611, 1986
A:Title: The primary structure of the putative oncogene pim-1 shows extensive homology v
A:Reference number: A24169; MUID:86272109; PMID:3015420
A:Accession: A24169
A:Molecule type: DNA
A:Residues: 1-313 <SEL>
A:Cross-references: UNIPROT:P06803; UNIPARC:UPI0000294AF; GB:M13945; GB:M13946; NID:920
C:Comment: Pim-1 autophosphorylates at unknown sites.
C:Genetics:
A:Gene: pim-1
A:Introns: 28/1; 63/3; 80/3; 203/1; 262/1
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; autophosphorylation; phosphotransferase; proto-oncogene; serine/threonin
F:36-290/Domain: protein kinase homology <KIN>
F:44-52/Region: protein kinase ATP-binding motif
F:67/Active site: Lys #status predicted

Query Match 94.7%; Score 1582; DB 1; Length 313;
Best Local Similarity 93.9%; Pred. No. 4.4e-72;
Matches 294; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNLDLHATKAPGKEPLESOYQVGPLLGGGFGSVYSGIRVSD 60
DB 1 MLLSKINSLAHLRAAPCNLDLHATKAPGKEPLESOYQVGPLLGGGFGSVYSGIRVAD 60
QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
DB 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
QY 121 ERPEPVQDLFDPIITRGALQOEELARSFQVQVLEAVRHCHNCVGLHRDIKDENILIDLNRG 180
DB 121 ERPEPVQDLFDPIITRGALQOEELARSFQVQVLEAVRHCHNCVGLHRDIKDENILIDLNRG 180
QY 181 ELKLDIFGSGALLKDTVTYDFDGTTRYVSPPEWIRVHRHGSAAVWSLGLLYDMVCGDI 240
DB 181 ELKLDIFGSGALLKDTVTYDFDGTTRYVSPPEWIRVHRHGSAAVWSLGLLYDMVCGDI 240
QY 241 PREHDEEIRGQVFRQVRVSSCOHLIRWCLALRPSDRPTFEEIQNHHPMQDVLPLQETA 300
DB 241 PREHDEEIRGQVFRQVRVSSCOHLIRWCLALRPSDRPTFEEIRNHHPMQDVLPLQAAS 300
QY 301 EHLHSLSPGSPK 313
DB 301 EHLHSLSPGSPK 313

RESULT 4

S55333
protein kinase pim-2 (BC 2.7.1.1.-) - mouse

Db 1339 RCVPKPTIIDDINNDKWL 1356

RESULT 11

T10449

probable serine/threonine-specific protein kinase (EC 2.7.1.1) - cucumber

N/Alternate names: SNF1-related protein kinase

C/Species: Cucumis sativus (cucumber)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-Oct-2004

C/Accession: T10449

R/Gumpel, N.J.

submitted to the EMBL Data Library, December 1996

A/Reference number: Z17020

A/Accession: T10449

A/Status: preliminary; translated from GB/EMBL/DBR3

A/Molecule type: mRNA

A/Residues: 1-504 <GUM>

A/Cross-references: UNIPROT:P93113; UNIPARC:UPI000004A4B92; EMBL:Y10036

A/Experimental source: cv. Masterpiece; cotyledon

C/Function:

A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-serine-phosphate

C/Superfamily: SNF1-related protein kinase; protein kinase homology

C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F/6-260/Domain: protein kinase homology <KIN>

Query Match 21.9%; Score 366; DB 2; Length 504;

Best Local Similarity 34.4%; Pred.No. 1.3e-11;

Matches 90; Conservative 51; Mismatches 105; Indels 16; Gaps 8

QY 38 YQVGLTGGGSGVSYGIRVSDNLPAIKHVEKDRISDNGELPNGTRVPMVVLKKVS 97

DB 8 YKLGTLTGISGKVKIAEHALTHGKVAIKILNRKIKN---LMEKVRREIKILRLFM 64

QY 98 SGFSGVIRLIDWFERPDSFVLIILERPFPQDLDFITERGALQELARSFQVLEAVRH 157

DB 65 --HPHILRYEVLETSDIYVMMEYKVS--GELFDYIVEKGRQLQDEARNFFQIISGVEY 121

QY 158 CHNCGVLHRDIKDENILIDNRGELKILIDFGSGALLKDTVYTPDF--GTRVYVSPPEWIRYH 216

DB 122 CHRMVNVHRLKPENLLLD--SKCNVKIADPGLSNIMRDGHFLKTS CGSPNYAAPEVISGK 180

QY 217 RYHGRSNAVKSLGILLYDMVCGDIPPEHDEI-----IRGOVF--PRQVVSSECOHLIRW 269

DB 181 LYAGPEVDVMSCGVILYALLCGTLPPF--DENIPLFKKIKGGIYVTLPSHLSSGARELIPS 239

QY 270 CLALRPSDRPTFEEIQNHPPMQ 291

DB 240 MLVVDPMKRITIPETIRQHPWFQ 261

RESULT 12

S52244

p69Eg3 protein - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004

C/Accession: S52244

R/Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.

submitted to the EMBL Data Library, October 1992

A/Description: Eg3, selected by differential screening encodes a new Xenopus protein

A/Reference number: S52243

A/Accession: S52244

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-651 <ROG>

A/Cross-references: UNIPROT:Q91821; UNIPARC:UPI000017A463; EMBL:Z17205; NID:960

C/Keywords: ATP

F/11-265/Domain: protein kinase homology <KIN>

F/19-27/Region: protein kinase ATP-binding motif

Query Match 21.6%; Score 361; DB 2; Length 651;

Best Local Similarity 34.8%; Pred.No. 2.8e-11;

Matches 94; Conservative 51; Mismatches 103; Indels 22; Gaps 8

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OM protein - protein search, using sw model

Run on: April 21, 2006, 12:50:45 ; Search time 189 Seconds
(without alignments)
727.648 Million cell updates/sec

Title: US-10-664-421-1

Perfect score: 1670

Sequence: 1 MLLSKINSLAHLRAAPCNDL.....LLPQETABIHLSLSPGPSK 313

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1670	100.0	313	5	ABP54943 Human Pim
2	1670	100.0	313	5	ABG33017 Human pro
3	1670	100.0	313	6	AAO19788 Human PIM
4	1670	100.0	313	7	ABU61613 Human PIM
5	1670	100.0	313	7	ABR62939 Human ser
6	1670	100.0	313	7	ABE55368 Human pro
7	1670	100.0	313	7	ADf45083 Human kin
8	1670	100.0	313	8	ADf45083 Human kin
9	1670	100.0	313	8	ADR88370 Human PIM
10	1670	100.0	313	8	ADP24227 PRO polyyp
11	1670	100.0	313	8	ADT07365 Human pro
12	1670	100.0	313	8	ADT14636 human Pim
13	1670	100.0	313	9	ADY86782 Human Pim
14	1670	100.0	313	9	AEA89424 Human Pim
15	1670	100.0	313	9	ABE96037 Human PIM
16	1657	99.2	313	2	AAW08139 Human cyt
17	1657	99.2	313	3	AAW87959 Human CR7
18	1657	99.2	313	8	ADL57202 Human PIM
19	1657	99.2	313	8	ADN03170 Human PIM
20	1657	99.2	313	9	ADY85580 Catalytic
21	1636	98.0	313	5	ABG33016 Rat prote
22	1636	98.0	313	6	AAO19789 Rat PIM1
23	1636	98.0	313	7	ABR62938 Rat serin
24	1636	98.0	313	9	ABE96039 Norway ra

25	1582	94.7	313	5	ABG33015	Abg33015	Mouse pro
26	1582	94.7	313	6	AAO19790	Aao19790	Murine P1
27	1582	94.7	313	7	ABR62940	Abre62940	Mouse ser
28	1582	94.7	313	8	ADN97347	Adn97347	Murine P1
29	1582	94.7	313	8	ADR88371	Adr88371	Mus muscu
30	1582	94.7	313	9	AEA19261	Aea19261	Mouse Pim
31	1582	94.7	313	9	ABE96041	Aeb96041	House mou
32	1576	94.4	313	9	AEA19263	Aea19263	Mouse Pim
33	1362	81.6	253	8	ADL57241	Adl57241	PIM1 domi
34	1296.5	77.6	257	2	AAy43942	Aay43942	Rat prote
35	1294.5	77.5	254	8	ADK71853	Adk71853	Human kin
36	1255	75.1	233	8	ADT07367	Adt07367	Human pro
37	1140	68.3	323	8	ADR88376	Adr88376	Colurnix
38	1135	68.0	326	2	AAy06886	Aay06886	KWHJ20 p
39	1135	68.0	374	8	ADX91611	Adx91611	Plant ful
40	1133	67.8	326	4	AAE29788	Aae29788	Human ser
41	1133	67.8	326	5	AAE23834	Aae23834	Human HKI
42	1133	67.8	326	5	ABG33011	Abg33011	Human ser
43	1133	67.8	326	7	ABR62932	Abre62932	Human pro
44	1133	67.8	326	8	ADJ96625	Adj96625	Human cal
45	1133	67.8	326	8	ADL97960	Adl97960	Human PIM

ALIGNMENTS

RESULT 1

ABP54943

ID ABP54943 standard; protein; 313 AA.

AC ABP54943;

XX 13-JAN-2003 (first entry)

DT Human Pim1.

DE Pim1; tyrosine threonine kinase; TTK; protein kinase; enzyme;

KW mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;

KW human; gene therapy.

XX Homo sapiens.

OS WO200268444-A1.

FN 06-SEP-2002.

XX 21-FEB-2002; 2002WO-US005278.

PF 21-FEB-2001; 2001US-0271254P.

PR (CHIR) CHIRON CORP.

XX Reinhard C, Jefferson AB, Chan VW;

XX WPI; 2002-698650/75.

XX N-PSDB; ABV73989.

Reducing growth of cancer cells comprises reducing Tyrosine Threonine Kinase (TTK) activity, useful in diagnosing and treating disorders with abnormal expression levels and activity of TTK, such as lung, colon, prostate and ovarian cancer.

Disclosure; Page 80-81; 113pp; English.

The present sequence is the protein sequence of human Pim1, a protein related to tyrosine threonine kinase (TTK, see ABP54938). TTK polynucleotides and polypeptides of the invention encompass polynucleotides and polypeptides having sequence similarity or sequence identity to human TTK and other genes and gene products related to TTK, such as Pim1. The invention is based on the finding that TTK is differentially expressed in various forms of cancer. It provides methods for the identification of cancerous cells, especially breast cancer and colon cancer cells, by detection of expression levels of TTK, as well as

CC diagnostic, prognostic and therapeutic methods. These methods can be used
CC as the basis of rational therapy. Assays for identifying molecules that
CC modulate the activity of these genes in cancers, as well as methods of
CC inhibiting tumour growth by inhibiting the activity of *tyr* are also
CC provided

SQ Sequence 313 AA;

Query Match 100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQVQVGLGSGFGSVYSGIRVSD 60
Db 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQVQVGLGSGFGSVYSGIRVSD 60

Qy 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFPERPDSFVLIL 120
Db 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFPERPDSFVLIL 120

Qy 121 ERPEPVQDLDFITFERGALQELARSPFWQVLEAVRHCHNGCVLHRDIKDNILIDLNRG 180
Db 121 ERPEPVQDLDFITFERGALQELARSPFWQVLEAVRHCHNGCVLHRDIKDNILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTFDGRVYSPPEWIRYHGRSAAVWSIGILLYDMVCGDI 240
Db 181 ELKLIDFGSGALLKDTVYTFDGRVYSPPEWIRYHGRSAAVWSIGILLYDMVCGDI 240

Qy 241 PFEHDEEIIIRQVFFRQVRSSECOHLIRWCIALRPSDRPTPEEIQNHPPWQDVLVLPQETA 300
Db 241 PFEHDEEIIIRQVFFRQVRSSECOHLIRWCIALRPSDRPTPEEIQNHPPWQDVLVLPQETA 300

Qy 301 EIHLSLSPGPSK 313
Db 301 EIHLSLSPGPSK 313

RESULT 2
ABG33017
ID ABG33017 standard; protein; 313 AA.
XX
AC ABG33017;
XX
DT 20-DEC-2002 (first entry)
XX
DE Human protein kinase phosphorylation site.
XX
KW HKID-1; serine/threonine kinase; cellular proliferative disorder;
KW differentiative disorder; cancer; haematopoietic neoplastic disorder;
KW Acute promyeloid leukaemia; APL; Chronic myelogenous leukaemia; CML;
KW Waldenstrom's macroglobulinaemia; WM; human.
XX
OS Homo sapiens.
XX
XX US2002115120-A1.
XX
PD 22-AUG-2002.
XX
XX 04-OCT-2001; 2001US-00971791.
XX
PF 26-JAN-1999; 99US-00237543.
XX
PR 23-AUG-2000; 2000US-00644450.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
PI Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;
XX
XX WPI; 2002-712471/77.

Modulating levels or activity of HKID-1 polypeptides, a member of
serine/threonine kinase superfamily, for treating cancer, by contacting
cell expressing the polypeptide with a modulator of the polypeptide.

PS Example 3; Page 40-41; 48pp; English.
XX The invention describes a method of modulating the level or activity of
human HKID-1 polypeptide, a member of serine/threonine kinase
superfamily. The method involves contacting a cell expressing the
polypeptide or nucleic acid with an agent to modulate the level or
activity of polypeptide, or level of nucleic acid molecule. The method is
useful for modulating the level or activity of HKID-1 polypeptide or
polynucleotide in a subject having or predisposed to having a disorder
involving cancer. Modulating HKID-1 expression or activity is useful for
therapeutic purposes, for treating cellular proliferation and/or
differentiative disorders including cancer or haematopoietic neoplastic
disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
amino acid sequence of a human protein kinase phosphorylation site

SQ Sequence 313 AA;

Query Match 100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQVQVGLGSGFGSVYSGIRVSD 60
Db 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQVQVGLGSGFGSVYSGIRVSD 60

Qy 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFPERPDSFVLIL 120
Db 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFPERPDSFVLIL 120

Qy 121 ERPEPVQDLDFITFERGALQELARSPFWQVLEAVRHCHNGCVLHRDIKDNILIDLNRG 180
Db 121 ERPEPVQDLDFITFERGALQELARSPFWQVLEAVRHCHNGCVLHRDIKDNILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTFDGRVYSPPEWIRYHGRSAAVWSIGILLYDMVCGDI 240
Db 181 ELKLIDFGSGALLKDTVYTFDGRVYSPPEWIRYHGRSAAVWSIGILLYDMVCGDI 240

Qy 241 PFEHDEEIIIRQVFFRQVRSSECOHLIRWCIALRPSDRPTPEEIQNHPPWQDVLVLPQETA 300
Db 241 PFEHDEEIIIRQVFFRQVRSSECOHLIRWCIALRPSDRPTPEEIQNHPPWQDVLVLPQETA 300

Qy 301 EIHLSLSPGPSK 313
Db 301 EIHLSLSPGPSK 313

RESULT 3
AAO19788
ID AAO19788 standard; protein; 313 AA.
XX
AC AAO19788;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human PIM1 kinase.
XX
KW Human; PIM1 kinase; PIM3 kinase; pain; analgesic.
XX
OS Homo sapiens.
XX
XX WO200293173-A2.
XX
PD 21-NOV-2002.
XX
XX 13-MAY-2002; 2002WO-EP005234.
XX
XX 11-MAY-2001; 2001DE-01023055.
XX
XX (CHEF) GRUENENTHAL GMBH.
XX
XX Weihe E, Schaefer MK;
XX


```
DR WPI; 2003-120715/11.
DR N-PSDB; ABZ69186.
XX
PT Method for identifying analgesics, useful particularly for treating
PT chronic pain, by screening compounds for interaction with PIM-1 or -3
PT kinase, or related compounds.
XX
PS Claim 1; Fig 1B; 97pp; German.
XX
XX The present invention relates to a method of identifying pain-regulating
CC compounds, involving screening candidate compounds for interaction with
CC PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC useful for treating chronic pain, particularly of neuropathic or
CC inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC neurodegenerative diseases). The present sequence is human PIM1 kinase
XX
XX Sequence 313 AA;
SQ
    Query Match      100.0%; Score 1670; DB 6; Length 313;
    Best Local Similarity 100.0%; Pred. No. 1.4e-154;
    Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEPLESQYQVGPLLGGSGFGSVYSGIRVSD 60
DB 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEPLESQYQVGPLLGGSGFGSVYSGIRVSD 60
QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
DB 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
QY 121 ERPEPVQDLFDFTIRGALQBELARSPFWQVLEAVRHCHNCGLVLRDIDENILIDLNRG 180
DB 121 ERPEPVQDLFDFTIRGALQBELARSPFWQVLEAVRHCHNCGLVLRDIDENILIDLNRG 180
QY 181 ELKLIDFGSGALLKDTVYTFDGTGVYSPPEWIRYHRYHGSAAVWSLGLLYDMVCGDI 240
DB 181 ELKLIDFGSGALLKDTVYTFDGTGVYSPPEWIRYHRYHGSAAVWSLGLLYDMVCGDI 240
QY 241 PFEHDEEIIIRGVFRQRVSSECOHLIRWCLALRPSDRPTFEEIQNHFWMQDVLPPQETA 300
DB 241 PFEHDEEIIIRGVFRQRVSSECOHLIRWCLALRPSDRPTFEEIQNHFWMQDVLPPQETA 300
QY 301 EIHLSLSPGPK 313
DB 301 EIHLSLSPGPK 313
RESULT 4
ABU61613
ID ABU61613 standard; protein; 313 AA.
XX
AC ABU61613;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human PIM1 protein.
XX
KW Human; tyrosine threonine kinase; TTK; cancer; cytostatic;
KW mitotic checkpoint gene; PIM1.
XX
OS Homo sapiens.
XX
FN US2003045491-A1.
XX
PD 06-MAR-2003.
XX
XX 21-FEB-2002; 2002US-00081119.
XX
PR 23-FEB-2001; 2001US-0289813P.
XX
PA (REIN/) REINHARD C.
PA (JEFF/) JEFFERSON A. B.
PA (CHAN/) CHAN V W.
```

```
XX Reinhard C, Jefferson AB, Chan VW;
PI
XX WPI; 2003-455566/43.
DR N-PSDB; ACA62265.
XX
PT Detecting cancer in a subject, by comparing expression levels of tyrosine
PT threonine kinase polypeptide or polynucleotide in a subject cell and a
PT normal cell, where an increase in the expression level in the test cell
PT is indicative of cancer.
XX
XX Disclosure; Page 34-35; 79pp; English.
XX
XX The invention relates to detecting cancer (other than ovarian cancer) in
XX a subject, comprising comparing the expression levels of tyrosine
XX threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or
XX polynucleotide in a test cell obtained from the subject and in a normal
XX non-cancer cell, where an increase in the expression level of TTK protein
XX or nucleic acid in the test cell compared to that in the normal cell,
XX indicates the presence of cancer other than ovarian cancer. Also included
XX are reducing growth of a cancerous cell (by contacting a cancerous cell
XX with an amount of an agent effective to reduce TTK polypeptide activity
XX in the cell), an assay for identifying a candidate agent that reduces
XX growth of a cancerous cell (comprising: (i) detecting the activity of a
XX TTK polypeptide in the presence of a candidate agent; and (ii) comparing
XX the activity of TTK polypeptide in the presence of a candidate agent
XX relative to TTK polypeptide activity in the absence of the candidate
XX agent), identifying an agent that reduces TTK activity (comprising: (i)
XX contacting a cancerous cell displaying elevated expression of a TTK-
XX encoding polynucleotide with a candidate agent; and (ii) determining the
XX effect of the candidate agent on TTK polypeptide activity) and assessing
XX the prognosis of a cancerous disease other than ovarian cancer in a
XX subject (comprising: (i) detecting expression of TTK -encoding
XX polynucleotide in a test cancer cell of a subject; and (ii) comparing a
XX level of expression of TTK-encoding polynucleotide in the test cancer
XX cell with a level of expression of the polynucleotide in a control non-
XX cancer cell, where the level of expression of TTK in the test cancer cell
XX relative to the level of expression in the control non-cancer cell is
XX indicative of the prognosis of the cancerous disease). The methods are
XX useful for detecting cancer (other than ovarian cancer) in a subject,
XX reducing growth of cancerous cells, identifying a candidate agent that
XX reduces growth of a cancerous cell, identifying an agent that reduces TTK
XX activity and assessing the prognosis of a cancerous disease other than
XX ovarian cancer. The methods are also useful for determining the ability
XX of a subject to respond to a particular therapy e.g. as a basis of
XX rational therapy. The present sequence represents a closely related
XX protein to human TTK, in this case human PIM1 (not defined)
XX
SQ Sequence 313 AA;
    Query Match      100.0%; Score 1670; DB 7; Length 313;
    Best Local Similarity 100.0%; Pred. No. 1.4e-154;
    Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEPLESQYQVGPLLGGSGFGSVYSGIRVSD 60
DB 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEPLESQYQVGPLLGGSGFGSVYSGIRVSD 60
QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
DB 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
QY 121 ERPEPVQDLFDFTIRGALQBELARSPFWQVLEAVRHCHNCGLVLRDIDENILIDLNRG 180
DB 121 ERPEPVQDLFDFTIRGALQBELARSPFWQVLEAVRHCHNCGLVLRDIDENILIDLNRG 180
QY 181 ELKLIDFGSGALLKDTVYTFDGTGVYSPPEWIRYHRYHGSAAVWSLGLLYDMVCGDI 240
DB 181 ELKLIDFGSGALLKDTVYTFDGTGVYSPPEWIRYHRYHGSAAVWSLGLLYDMVCGDI 240
QY 241 PFEHDEEIIIRGVFRQRVSSECOHLIRWCLALRPSDRPTFEEIQNHFWMQDVLPPQETA 300
DB 241 PFEHDEEIIIRGVFRQRVSSECOHLIRWCLALRPSDRPTFEEIQNHFWMQDVLPPQETA 300
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Qy	301	EIHLHSLSPGSPK 313	181	ELKLIDFGSGALLKDTVTYDPTGTRVYSPPEWIRVHRVYHGRSAAVWSLGLLYDMVCGDI	240
Db	301	EIHLHSLSPGSPK 313	181	ELKLIDFGSGALLKDTVTYDPTGTRVYSPPEWIRVHRVYHGRSAAVWSLGLLYDMVCGDI	240
ABR62939			241	PFEHDEEIIIRGQVFFRQVRVSSECQHLIRWCIALRPSDRPTFEEIQNHPPMDVLLPQETA	300
RESULT 5			241	PFEHDEEIIIRGQVFFRQVRVSSECQHLIRWCIALRPSDRPTFEEIQNHPPMDVLLPQETA	300
ID	ABR62939	standard; protein; 313 AA.	301	EIHLHSLSPGSPK 313	
XX	AC	ABR62939;	301	EIHLHSLSPGSPK 313	
XX	DT	04-DEC-2003 (first entry)			
XX	XX	Human serine/threonine protein kinase PIM-1.			
DE	XX	Human; PIM-1; protein kinase; enzyme.			
XX	XX	Homo sapiens.			
XX	XX	WO2003060130-A2.			
XX	PD	24-JUL-2003.			
XX	XX	20-JAN-2003; 2003WO-EP000492.			
XX	PP	19-JAN-2002; 2002EP-00001401.			
XX	PR	(AVET) AVENTIS PHARMA DEUT GMBH.			
XX	PA	Korn M, Mueller G, Schneider R, Tschank G;			
XX	PI	WPI; 2003-598536/56.			
XX	DR	New human or murine PIM-3 DNAs or polypeptides, useful for as a screening agent for identifying anti-type 2 diabetes mellitus drugs, or for treating insulin resistance or type 2 diabetes mellitus.			
XX	PT	Example 2; Page 40; 40pp; English.			
PS	XX	The present sequence is the protein sequence of the human serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins are the paralogues of novel human and murine PIM-3 proteins (see ABR62932 and ABR62933) of the invention, which are therefore expected to be involved in cancer and cell growth regulation. PIM-3 is also involved in the development of insulin resistance and type 2 diabetes mellitus. The invention relates to the use of PIM-3 nucleic acids and proteins in: screening assays for compounds that modulate insulin resistance or type 2 diabetes mellitus; detection assays for detecting insulin resistance or type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing, forensic biology); predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, pharmacogenomics); and for the preparing a medicament for the treatment of insulin resistance or type 2 diabetes mellitus			
XX	XX	Sequence 313 AA;			
SQ					
		Query Match			
		Best Local Similarity 100.0%; Score 1670; DB 7; Length 313;			
		Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MLLSKINSLAHLRAAPCNLDLHATKLAPGKEPELESQVQGPLGSGFGVSGYGRVSD	60		
Db	1	MLLSKINSLAHLRAAPCNLDLHATKLAPGKEPELESQVQGPLGSGFGVSGYGRVSD	60		
Qy	61	NLPVAIKHVEKDRISDMGELPNGTRVPMVLLKKVSSGFSVIRLLDWFERPDSFVLIL	120		
Db	61	NLPVAIKHVEKDRISDMGELPNGTRVPMVLLKKVSSGFSVIRLLDWFERPDSFVLIL	120		
Qy	121	ERPEPVQDLFDITFERGALQELARSFPWQVLEAVRHCHNGCVLHRDIDKENILIDLNRG	180		
Db	121	ERPEPVQDLFDITFERGALQELARSFPWQVLEAVRHCHNGCVLHRDIDKENILIDLNRG	180		

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX
 XX Sequence 313 AA;

Query Match 100.0%; Score 1670; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 1.4e-154;
 Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEKEPLESQVQVGLGSGFGSVYSGIRVSD 60
 DB 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEKEPLESQVQVGLGSGFGSVYSGIRVSD 60
 QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
 DB 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
 QY 121 ERPEPVQDLFPDITRGALQELARSPFWQVLEAVRHCHNCGLVLRDIDKENILIDLNRG 180
 DB 121 ERPEPVQDLFPDITRGALQELARSPFWQVLEAVRHCHNCGLVLRDIDKENILIDLNRG 180
 QY 181 ELKLIDFGSGALLKDTVTYDFDGTGVYSPPEWIRVHRHGSAAVWSLGLLYDMVCGDI 240
 DB 181 ELKLIDFGSGALLKDTVTYDFDGTGVYSPPEWIRVHRHGSAAVWSLGLLYDMVCGDI 240
 QY 241 PFEHDEEIRGQVFRQVRVSSCOHLIRWCLALRPSDRPTPEEIQNHPMQDVLVLPQETA 300
 DB 241 PFEHDEEIRGQVFRQVRVSSCOHLIRWCLALRPSDRPTPEEIQNHPMQDVLVLPQETA 300
 QY 301 EIHLSLSPGSPK 313
 DB 301 EIHLSLSPGSPK 313

RESULT 7

ADF45083
 ID ADF45083 standard; protein; 313 AA.

AC ADF45083;

DT 12-FEB-2004 (first entry)

DE Human kinase PIM1.

KW Human; protein kinase; enzyme; inhibitor; PIM1.

OS Homo sapiens.

PN WO2003081210-A2.

PD 02-OCT-2003.

XX 20-MAR-2003; 2003WO-US008725.

PF 21-MAR-2002; 2002US-0366892P.

PR (SUNE-) SUNESIS PHARM INC.

PA Prescott JC, Braisted A;

XX WPI; 2003-865136/80.

XX Identifying ligand binding to inactive conformation of target protein
 PT kinase (T) comprises contacting the conformation modified (T) which
 PT contains reactive group at binding site, with ligands and detecting
 PT kinase-ligand conjugate formation.

PS Disclosure; SEQ ID NO 52; 260pp; English.

XX

CC The present invention relates to a method for identifying a ligand (L),
 CC which binds to an inactive conformation of target protein kinase (T). The
 CC method involves contacting inactive conformation of (T), which contains
 CC or is modified to contain a reactive group at or near a binding site of
 CC interest, with one or more ligand candidates capable of covalently
 CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
 CC The method is useful for identifying protein kinase inhibitors that
 CC preferentially bind to inactive conformation of a target protein kinase.
 CC The present sequence is a protein kinase which may be modified via an
 CC amino acid substitution, for use in the method of the invention.

XX
 XX Sequence 313 AA;

Query Match 100.0%; Score 1670; DB 7; Length 313;

Best Local Similarity 100.0%; Pred. No. 1.4e-154;

Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEKEPLESQVQVGLGSGFGSVYSGIRVSD 60

DB 1 MLLSKINSLAHLRAAPCNDLHATKAPGKEKEPLESQVQVGLGSGFGSVYSGIRVSD 60

QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120

DB 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120

QY 121 ERPEPVQDLFPDITRGALQELARSPFWQVLEAVRHCHNCGLVLRDIDKENILIDLNRG 180

DB 121 ERPEPVQDLFPDITRGALQELARSPFWQVLEAVRHCHNCGLVLRDIDKENILIDLNRG 180

QY 181 ELKLIDFGSGALLKDTVTYDFDGTGVYSPPEWIRVHRHGSAAVWSLGLLYDMVCGDI 240

DB 181 ELKLIDFGSGALLKDTVTYDFDGTGVYSPPEWIRVHRHGSAAVWSLGLLYDMVCGDI 240

QY 241 PFEHDEEIRGQVFRQVRVSSCOHLIRWCLALRPSDRPTPEEIQNHPMQDVLVLPQETA 300

DB 241 PFEHDEEIRGQVFRQVRVSSCOHLIRWCLALRPSDRPTPEEIQNHPMQDVLVLPQETA 300

QY 301 EIHLSLSPGSPK 313

DB 301 EIHLSLSPGSPK 313

RESULT 8

ADOL9690
 ID ADOL9690 standard; protein; 313 AA.

XX ADOL9690;

DT 12-AUG-2004 (first entry)

XX Human PRO polypeptide #308.

XX Human; PRO; immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.

OS Homo sapiens.

PN WO2004043361-A2.

XX 27-MAY-2004.

PD 06-NOV-2003; 2003WO-US035268.

PF 08-NOV-2002; 2002US-0425235P.

XX (GETH) GENENTECH INC.

XX

PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
FI Wood WI, Wu TD;
XX WPI; 2004-420067/39.
DR N-PSDB; ADOI9689.
XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthritis.
XX Claim 7; SEQ ID NO 616; 1731pp; English.
XX
XX The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polypeptide of the
CC invention.
XX
SQ Sequence 313 AA;
Query Match 100.0%; Score 1670; DB 8; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQYQVGLGSGFGSVYSGIRVSD 60
Db 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQYQVGLGSGFGSVYSGIRVSD 60
Qy 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFRRPDSFVLIL 120
Db 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFRRPDSFVLIL 120
Qy 121 ERPEPVQDLFDFTFIRGALQELARSPFWQVLEAVRHCHNCVLRHDIKDNILIDLNRG 180
Db 121 ERPEPVQDLFDFTFIRGALQELARSPFWQVLEAVRHCHNCVLRHDIKDNILIDLNRG 180
Qy 181 ELKIDFGSGALLKDTVTYDFDGTGRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240
Db 181 ELKIDFGSGALLKDTVTYDFDGTGRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240
Qy 241 PFEHDEEIIIRGOVFRQRVSSECOHLIRWCLALRPSDRPTEETIQRHPWMDVLLPQETA 300
Db 241 PFEHDEEIIIRGOVFRQRVSSECOHLIRWCLALRPSDRPTEETIQRHPWMDVLLPQETA 300
Qy 301 EIHLSLSPGPSK 313
Db 301 EIHLSLSPGPSK 313
RESULT 9
ADR88370
ID ADR88370 standard; protein; 313 AA.
XX-4 ADR88370;
XX
XX 18-NOV-2004 (first entry)
DT Human PIM 1 protein.
DE
XX Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW G-protein coupled receptor; methyl transferase; ligase; PIM; human.
XX
XX Homo sapiens.
XX
XX US2004171062-A1.

XX 02-SEP-2004.
PD
XX 28-FEB-2003; 2003US-00377268.
PF
XX 28-FEB-2002; 2002US-0360651P.
PR 16-SEP-2002; 2002US-0411398P.
PR 20-SEP-2002; 2002US-0412341P.
PR 02-JAN-2003; 2003US-0437929P.
XX (PLEX-) PLEXIKON INC.
PA
PI Hirth K, Milburn MW;
PI WPI; 2004-642017/62.
XX
XX Designing a ligand binding to a target molecule, comprises identifying as
PT molecular scaffolds compounds binding to members of a molecular family,
PT detecting orientation of scaffolds at a binding site of target, and
PT synthesizing ligand.
XX
XX Disclosure; SEQ ID NO 9; 186pp; English.
XX
XX The present invention relates to a method of designing a ligand binding
CC to a target molecule. The method involves identifying as molecular
CC scaffolds compounds binding to members of a molecular family, detecting
CC orientation of scaffolds at a binding site of target, and synthesizing
CC ligand. The invention is useful for designing drug products and for
CC designing ligand binding to target molecules such as nuclear hormone
CC receptors, TNF receptors, G-protein coupled receptors, methyl
CC transferases, ligases, etc. The present sequence is the human PIM 1
CC protein. This sequence is used to illustrate the method of invention.
XX
SQ Sequence 313 AA;
Query Match 100.0%; Score 1670; DB 8; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQYQVGLGSGFGSVYSGIRVSD 60
Db 1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQYQVGLGSGFGSVYSGIRVSD 60
Qy 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFRRPDSFVLIL 120
Db 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFRRPDSFVLIL 120
Qy 121 ERPEPVQDLFDFTFIRGALQELARSPFWQVLEAVRHCHNCVLRHDIKDNILIDLNRG 180
Db 121 ERPEPVQDLFDFTFIRGALQELARSPFWQVLEAVRHCHNCVLRHDIKDNILIDLNRG 180
Qy 181 ELKIDFGSGALLKDTVTYDFDGTGRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240
Db 181 ELKIDFGSGALLKDTVTYDFDGTGRVYSPPEWIRYHRYHGRSAAVWSLIGILLYDMVCGDI 240
Qy 241 PFEHDEEIIIRGOVFRQRVSSECOHLIRWCLALRPSDRPTEETIQRHPWMDVLLPQETA 300
Db 241 PFEHDEEIIIRGOVFRQRVSSECOHLIRWCLALRPSDRPTEETIQRHPWMDVLLPQETA 300
Qy 301 EIHLSLSPGPSK 313
Db 301 EIHLSLSPGPSK 313
RESULT 10
ADP24227
ID ADP24227 standard; protein; 313 AA.
XX
XX AC ADP24227;
XX
XX 18-NOV-2004 (first entry)
DT
XX
XX PRO polypeptide SEQ ID NO:1405.
DE

XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
 XX Unidentified.
 OS
 PN WO2004041170-A2.
 XIR 21-MAY-2004.
 PD 30-OCT-2003; 2003WO-US034312.
 XX 01-NOV-2002; 2002US-0423394P.
 XX (GETH) GENENTECH INC.
 XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
 PI Wu TD;
 XX WPI; 2004-419628/39.
 DR N-PSDB; ADP24226.
 XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 XX Claim 7; SEQ ID NO 1405; 2940pp; English.
 XX The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 XX
 SQ Sequence 313 AA;
 Query Match 100.0%; Score 1670; DB 8; Length 313;
 Best Local Similarity 100.0%; Pred. No. 1.4e-154;
 Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLLSKINSLAHRAAPCNDLHATKLPCKEKEPLESQYQVGLLGGSGFGSVYGIKVSVD 60
 Db 1 MLLSKINSLAHRAAPCNDLHATKLPCKEKEPLESQYQVGLLGGSGFGSVYGIKVSVD 60
 Qy 61 NLPVAKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVILL 120
 Db 61 NLPVAKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVILL 120
 Qy 121 ERPEPVQDLFDFTIRGALQBELARSFFWQVLEAVRHCHNCVGLHRDKENILIDLNRG 180

Db 121 ERPEPVQDLFDFTIRGALQBELARSFFWQVLEAVRHCHNCVGLHRDKENILIDLNRG 180
 Qy 181 ELKLIDFGSGALLKDTVTYDFDGTTRVYSPPEWIRYHRVHGRSAAVWSLGILLYDMVCGDI 240
 Db 181 ELKLIDFGSGALLKDTVTYDFDGTTRVYSPPEWIRYHRVHGRSAAVWSLGILLYDMVCGDI 240
 Qy 241 PPEHDEEIIIRGVPRQRVSSECOHLIRWCALRPSDRPTFEIIONHPMMQDVLVPOETA 300
 Db 241 PPEHDEEIIIRGVPRQRVSSECOHLIRWCALRPSDRPTFEIIONHPMMQDVLVPOETA 300
 Qy 301 EIHLSLSPGSPK 313
 Db 301 EIHLSLSPGSPK 313
 RESULT 11
 ADT07365
 ID ADT07365 standard; protein; 313 AA.
 XX AC ADT07365;
 XX DT 13-JAN-2005 (first entry)
 XX DE Human protein #1 associated to anticancer compound screening method.
 XX KW Prophylactic-therapeutic agent; apoptosis inducing agent;
 KW anticancer agent; serine/threonine kinase Pim-1; cancer; solid tumour;
 KW human.
 XX OS Homo sapiens.
 XX PN WO2004090158-A1.
 XX PD 21-OCT-2004.
 XX PF 05-APR-2004; 2004WO-JP004917.
 XX PR 03-APR-2003; 2003US-0459644P.
 XX PA (ONCO-) ONCOREX INC.
 XX PI Kobayashi M, Jian C;
 XX WPI; 2004-748778/73.
 DR N-PSDB; ADT07366.
 XX Screening for a prophylactic-therapeutic apoptosis inducing agent or
 PT enhancer of anticancer agent, comprises use of serine/threonine kinase
 PT Pim-1, its partial peptide or its salt.
 XX Disclosure; SEQ ID NO 1; 93pp; Japanese.
 XX The invention relates to a method of screening a prophylactic-therapeutic
 CC agent for an apoptosis inducing agent or an enhancer of an anticancer
 CC agent. The method involves the use of a serine/threonine kinase Pim-1,
 CC its partial peptide or its salt. Also disclosed is a kit for carrying out
 CC the method of the invention. The method is useful for screening a
 CC prophylactic-therapeutic agent for cancer. The method is also useful for
 CC patient having a solid tumour that is resistant to an anticancer agent
 CC (induced by hypoxia), and for screening a substance that promotes or
 CC inhibits the activity of serine/threonine kinase Pim-1. The present
 CC sequence represents a human polypeptide relating to the present
 CC invention.
 XX
 SQ Sequence 313 AA;
 Query Match 100.0%; Score 1670; DB 8; Length 313;
 Best Local Similarity 100.0%; Pred. No. 1.4e-154;
 Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLLSKINSLAHRAAPCNDLHATKLPCKEKEPLESQYQVGLLGGSGFGSVYGIKVSVD 60

Db 1 MLLSKINLAHLRAAPCNDLHATKAPCKEKEPLESQVQVGLLGGSGFGSVYSGIRVSD 60
Qy 61 NLPVAKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSGVIRLLDWFRRPDSFVLIL 120
Db 61 NLPVAKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSGVIRLLDWFRRPDSFVLIL 120
Qy 121 ERPEPVQDLFDFTIRGALQELARSPFWQVLEAVRHCHNCGLVLRDIDKDNILIDLNRG 180
Db 121 ERPEPVQDLFDFTIRGALQELARSPFWQVLEAVRHCHNCGLVLRDIDKDNILIDLNRG 180
Qy 181 ELKLIDFGSGALLKDTVTYDGTGVYSPPEWIRVHRVHGRSAAVWSLIGILLYDMVCGDI 240
Db 181 ELKLIDFGSGALLKDTVTYDGTGVYSPPEWIRVHRVHGRSAAVWSLIGILLYDMVCGDI 240
Qy 241 PFEHDEEIIIRGVFRQVRSSECOHLIRWCLALRPSDRPTFEEIQNHHPMDVLLPQETA 300
Db 241 PFEHDEEIIIRGVFRQVRSSECOHLIRWCLALRPSDRPTFEEIQNHHPMDVLLPQETA 300
Qy 301 EIHLSLSLSPGPSK 313
Db 301 EIHLSLSLSPGPSK 313

RESULT 12
ADT14636
ID ADT14636 standard; protein; 313 AA.
XX
AC ADT14636;
XX
DT 13-JAN-2005 (first entry)
XX
DE human Pim-1 (oncogene-encoded serine/threonine kinase) protein.
XX
KW crystallography; Pim-1; cancer; serine/threonine kinase; enzyme;
KW protein co-ordinate data; protein structure.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH Domain 33..121
FT Domain /note = N-terminal domain
FT Domain 44..52
FT Domain /note = Glycine-rich loop
FT Domain 122..127
FT Domain /note = Hinge region
FT Domain 128..305
FT Domain /note = C-terminal domain
FT Modified-site 166
FT /label= OTHER
FT /note= "OTHER = Forms a salt bridge via linkage to
FT Asp200"
FT Domain 186..210
FT /note = Activation loop
FT Modified-site 200
FT /label= OTHER
FT /note= "OTHER = Forms a salt bridge via linkage to
FT Arg166"
XX
PN WO2004090106-A2.
XX
PD 21-OCT-2004.
XX
XX 01-APR-2004; 2004WO-US010345.
XX
XX 04-APR-2003; 2003US-0460843P.
XX
XX 12-MAR-2004; 2004US-0552526P.
XX
XX (VERT-) VERTEX PHARM INC.
XX
XX Jacobs ML, Hare B, Swenson L;
XX
XX WPI; 2004-757977/74.

XX Crystal useful for developing Pim-1 (oncogene-encoded serine/threonine
PT kinase) inhibitors, comprises human Pim-1 protein, Pim-1 homologue, human
PT Pim-1 protein complex, or Pim-1 homologue complex.
XX
XX Claim 8; SEQ ID NO 2; 219pp; English.
XX
CC The invention relates to a novel crystal comprising a human Pim-1
CC (oncogene-encoded serine/threonine kinase) protein, a Pim-1 homologue, a
CC human Pim-1 protein complex or a Pim-1 homologue complex. Pim-1 is
CC primarily expressed in haemopoietic and germ cell lines and this
CC expression is tightly regulated and induced by cytokines, mitogens and
CC hormones. Human Pim-1 is associated with multiple cellular functions,
CC such as proliferation, differentiation, apoptosis and tumorigenesis. The
CC crystal of the invention relates particularly to the residues involved in
CC the active site and binding sites of Pim-1. Such information may be
CC useful for developing Pim-1 inhibitors that are useful as therapeutic
CC agents in the treatment of cancer. The current sequence is that of the
CC human Pim-1 (oncogene-encoded serine/threonine kinase) protein of the
CC invention.
XX
XX Sequence 313 AA;
SQ
Query Match 100.0%; Score 1670; DB 8; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLLSKINLAHLRAAPCNDLHATKAPCKEKEPLESQVQVGLLGGSGFGSVYSGIRVSD 60
Db 1 MLLSKINLAHLRAAPCNDLHATKAPCKEKEPLESQVQVGLLGGSGFGSVYSGIRVSD 60
Qy 61 NLPVAKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSGVIRLLDWFRRPDSFVLIL 120
Db 61 NLPVAKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSGVIRLLDWFRRPDSFVLIL 120
Qy 121 ERPEPVQDLFDFTIRGALQELARSPFWQVLEAVRHCHNCGLVLRDIDKDNILIDLNRG 180
Db 121 ERPEPVQDLFDFTIRGALQELARSPFWQVLEAVRHCHNCGLVLRDIDKDNILIDLNRG 180
Qy 181 ELKLIDFGSGALLKDTVTYDGTGVYSPPEWIRVHRVHGRSAAVWSLIGILLYDMVCGDI 240
Db 181 ELKLIDFGSGALLKDTVTYDGTGVYSPPEWIRVHRVHGRSAAVWSLIGILLYDMVCGDI 240
Qy 241 PFEHDEEIIIRGVFRQVRSSECOHLIRWCLALRPSDRPTFEEIQNHHPMDVLLPQETA 300
Db 241 PFEHDEEIIIRGVFRQVRSSECOHLIRWCLALRPSDRPTFEEIQNHHPMDVLLPQETA 300
Qy 301 EIHLSLSLSPGPSK 313
Db 301 EIHLSLSLSPGPSK 313
RESULT 13
ADY86782
ID ADY86782 standard; protein; 313 AA.
XX
AC ADY86782;
XX
DT 02-JUN-2005 (first entry)
XX
DE Human Pim1 protein, SEQ ID NO: 18.
XX
KW Prognosis; cancer; cytostatic; neoplasm; tyrosine threonine kinase; TTK;
KW Pim1.
XX
OS Homo sapiens.
XX
XX US2005063974-A1.
XX
XX 24-MAR-2005.
XX
XX 27-SEP-2004; 2004US-00951477.
XX
XX

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PR 21-FEB-2001; 2001US-0271254P.
PR 23-FEB-2001; 2001US-0289813P.
PR 21-FEB-2002; 2002US-00081119.
XX
PA (REIN/) REINHARD C.
PA (JEFF/) JEFFERSON A B.
PA (CHAN/) CHAN V W.
XX
PX Reinhard C, Jefferson AB, Chan VW;
XX
XX WPI; 2005-241248/25.
DR N-PSDB; ADY86781.
XX
XX Assessment of prognosis of a cancerous disease other than ovarian cancer
PT comprises detection and comparison of expression of a tyrosine threonine
PT kinase-encoding polynucleotide in a test cancer cell with a control non-
PT cancer cell.
XX
XX Disclosure; SEQ ID NO 18; 78pp; English.
XX
XX The invention relates to a method for assessing the prognosis of a
CC cancerous disease other than ovarian cancer which involves detection and
CC comparison of expression of a tyrosine threonine kinase (TTK)-encoding
CC polynucleotide in a test cancer cell with a control non-cancer cell. The
CC method is useful to assess the prognosis of a cancerous disease other
CC than ovarian cancer. It is useful to identify cancerous cells and to
CC determine the ability of a subject to respond to a particular therapy
CC e.g. as the basis of rational therapy. The present sequence is the TTK
CC related human Pim1 protein.
XX
SQ Sequence 313 AA;
Query Match 100.0%; Score 1670; DB 9; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVSD 60
DB 1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVSD 60
QY 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
DB 61 NLPVAIKHVEKDRISDWGELPNGTRVPMVEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
QY 121 ERPEPVQDLFDFTTGERGALQBELARSPFWQVLEAVRHCHNCVGLHRDKDENILIDLNRG 180
DB 121 ERPEPVQDLFDFTTGERGALQBELARSPFWQVLEAVRHCHNCVGLHRDKDENILIDLNRG 180
QY 181 ELKLIDFGSGALLKDTVTYDFDGTTRVYSPPEWIRYHRHGSAAVWSLGLLYDMVCGDI 240
DB 181 ELKLIDFGSGALLKDTVTYDFDGTTRVYSPPEWIRYHRHGSAAVWSLGLLYDMVCGDI 240
QY 301 EIHLSLSPGSK 313
DB 301 EIHLSLSPGSK 313
RESULT 14
AEA89424
ID AEA89424 standard; protein; 313 AA.
AC AEA89424;
XX
XX 25-AUG-2005 (first entry)
XX Human Pim1 protein, SEQ ID NO: 18.
XX
XX Drug screening; diagnosis; therapeutic; cancer; cytostatic; neoplasm;
KW Pim1.
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Db      241 PFEHDEIIRGVFRQVRSSECQHLIRWCLALRPSDRPTFEEIQNHFWMDVLLPQETA 300
Qy      301 EIHLSLSPGSPK 313
      |||||
Db      301 EIHLSLSPGSPK 313
      |||||

RESULT 15
ID      AEB96037 standard; protein; 313 AA.
XX
AC      AEB96037;
XX
DT      20-OCT-2005 (first entry)
XX
DE      Human PIM-1 serine-threonine kinase protein.
XX
KW      micturition disorder; urinary dysfunction; uropathic; gene therapy;
KW      PIM-1 protein kinase; serine-threonine kinase; enzyme.
XX
OS      Homo sapiens.
XX
PN      DE102004004894-A1.
XX
PD      18-AUG-2005.
XX
PF      30-JAN-2004; 2004DE-10004894.
XX
PR      30-JAN-2004; 2004DE-10004894.
XX
PA      (CHEF ) GRUENENTHAL GMBH.
XX
PI      Christoph T;
XX
DR      WPI; 2005-556609/57.
DR      N-PSDB; AEB96036.
DR      REFSEQ; NP_002639.
XX

Identifying substances that regulate PIM kinases, useful for treatment
and diagnosis of urinary incontinence and the urge to urinate, and
similar use of PIM proteins or nucleic acids.

Claim 1; Fig 1B; 37pp; German.

The invention relates to a novel method for identifying substances that
regulate urinary incontinence and the urge to urinate. The method
comprises incubating a test compound with a cell and/or cell preparation
that has synthesized a specific protein of the PIM (proviral integration
site) kinase family and measuring either binding of the test compound to
the PIM kinase, or a functional parameter that is altered by the binding.
The method of the invention demonstrates uropathic and gene therapy
applications and may be useful for treatment and diagnosis of urinary
incontinence and the urge to urinate. The method is based upon regulating
the activity or expression of PIM kinases that are involved in bladder
control. The current sequence is that of the human PIM-1 serine-threonine
kinase protein of the invention.
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Query Match      100.0%; Score 1670; DB 9; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQYQVGPLLGSGFGSGVSGIRVSD 60
Db      1 MLLSKINSLAHLRAAPCNDLHATKLPAGEKEPLESQYQVGPLLGSGFGSGVSGIRVSD 60

Qy      61 NLPVAIKHVKDRISDWGELPENGTRVPMNEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120
Db      61 NLPVAIKHVKDRISDWGELPENGTRVPMNEVLLKKVSSGFGSVIRLLDWFERPDSFVLIL 120

Qy      121 ERPEPVQDLFDFFITERGALQBELARSPFWQVLEAVRHCHNCQVLRHDIKDNILIDLNRG 180
```

Search completed: April 21, 2006, 12:54:03
Job time : 192 secs